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Result
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Listing first 45 summaries
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Maximum DB
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1: geneseqp1990
2: geneseqp2000
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5: geneseqp2002
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2006 Compugen Ltd.
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AAB065509
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Aab01622 Discosoma
Aag65509 Anthozoan
Abb08834 Yeast opt
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1207	1207	1207	1208	1208	1208	1208	1209	1209	1209	1209	1210	1210	1210	1210	1210	1210	1211	1211	1211	1211
99.4	99.4	99.4	99.5	99.5	99.5	99.5	99.6	99.6	99.6	99.6	99.7	99.7	99.7	99.7	99.7	99.7	99.8		99.8	99.8
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ADY51734	AAE17541	AAE28921	ADH34500	ABW00939	ABW00935	ABW00932	ABB08835	ABW00931	ABW00936	AAE28922	ADL18156	ADL18132	ADE24109	AAG65510	ABW00930	AAE28919	ADH34499	ADH34498	ABW00938	ABW00929
Ady51734 Discosoma	٠.	-							-				_							

## ALIGNMENTS

## RRESULT 1 AAY99836 ID AAY99 XX 228 AC AAY9 AC AAY9 XX 112-S DT 112-S DT 112-S DT 112-S DT 113-S XX Anth XW Anth XW Anth XW Fluo XX Anth XX I1-I PR 11-I PR 11-/note= Misc-difference 127 Discosoma sp; "red". Discosoma sp. 12-SEP-2003 19-SEP-2000 AAY99836; AAY99836 standard; protein; 225 AA. Lukyanoy SA, Ding L; key Location/Qualifiers Misc-difference 122 Anthozoa; drFP583; fluorescent protein; non-bioluminescent organism; fluorescent labeling. Novel fluorescent protein from non-bioluminescent Discosoma useful for fluorescent labeling and as markers. 11-DEC-1998; 14-OCT-1999; 10-DEC-1999; WO200034326-A1 Claim 20; Page 74-75; 86pp; English. WPI; 2000-423381/36. 15-JUN-2000. (CLON-) CLONTECH LAB INC. (revised) (first entry) "red" novel fluorescent protein drFP583 Fradkov AF, 98US-00210330 99US-00418529 99WO-US029473 /note= "encoded by GTTG" "encoded by TC" Labas YA, Matz MV, Green တ Chen вþ. Υ. red,

Adq28780 Adx26534 Abb08821

Discosoma
Discosoma
Wild-type
Discosoma
D sp red
Jellyfish
Discosoma
Autofluor
Autofluor
Autofluor

Discosoma

The present sequence is a novel fluorescent protein (nFP) encoded by the full-length cDNA drFP583. drFP583 was isolated from Discosoma sp. "red", a non-bioluminescent species of the Class Anthozoa. Fluorescent proteins can be used in fluorescent labeling, a useful tool for marking a protein

Adh34489 Adl46203 Adn33979 Abw00918 Adf70403

Discosoma Discosoma

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Abbo8834 Yeast opt Aae28833 Discosoma Aae17540 Discosoma Aao18270 Discosoma Ady51716 Discosoma Ade34962 Discosoma Adc24126 Discosoma

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                                                                          Claim 3; Page 68-69; 73pp; English
                                                                                                                              Novel method for identifying from non-bioluminescent Antho labeling and as markers.
                                                                                                                                                                                                                                                                                                                     Lukyanoy SA,
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                                                                                                                                                                                                                                                                                                                                                                                   CLONTECH LAB INC.
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szoa which are useful for fluorescent
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The present sequence is Discosoma sp.

red fluorescent protein drFP583.

The invention provides a nucleic acid CC protein (II) that differs from the

encoding sequence

functional red fluorescent of an Anthozoan red

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RESULT 3
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was isolated using the Aequoria victoria green fluorescent protein (GFP) sequence, which was used to design PCR primers which might isolate other fluorescent proteins from a number of species of Anthozoa. These were Anemonia majano, Clavularia sp., Zoanthus sp., Discosoma sp. and Anemonia sulcata. The CDNA obtained was then screened in the search for sequences encoding fluorescent proteins. The other proteins found in this manner were cFP484, zFP506, zFP538, amFP486, dsFP483, asFP600, dgFP512 and dmFP592. These proteins can be used as fluorescent labels (for gene expression and protein localisation studies and in fluorescence resonance energy transfer (FRET) studies) in place of fluorophore derivatives and luciferases, as these involve laborious processes and the latter require cofactors. They can also be used in place of GFP, which is too stable to be useful when studying short-term or repetitive events
                                                                              Proteins for Fluorescence Resonance Energy Transfer (FRET) comprise functional red fluorescent proteins, and the encoding nucleic acids key mutations for improving the proteins function.
                                                                                                                                                                                                                                                                                                                30-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                               Fluorescent
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                                               Disclosure;
                                                                                                                                                WPI; 2001-557704/62.
                                                                                                                                                                                                               (AURO-) AURORA BIOSCIENCES CORP
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                                                                                                                                                                               Zamaira E,
                                               Page
                                                                                                                                                                                                                                                                                                                                                                                                             protein; Anthozoan; fluorescence; marker; FRET; red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               fluorescent
                                                                            fluorescent proteins, and for improving the proteins
                                               85; 90pp; English
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Pred. No. 1e-127;
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                                                                                                nucleic acids,
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Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fluorescent protein by at least one amino acid substitution, and with different fluorescent properties. The red fluorescent protein of the invention can be expressed by standard recombinant methodology. (II) are used a fluorescent markers and FRET partners. It is used for identifying protein-protein interactions. (II) is also suitable for multiplexed fluorescent proteins. (II) has improved brightness, reduced spectral cross talk, and is rapidly and efficiently expressed in mammalian cells. The key mutations in the encoding nucleic acids provide improved folding, brightness, and create (II) with sharper, more defined excitation and emission peaks when expressed in mammalian cells. The present sequence represents an anthozoan fluorescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                          Yeast; red fluorescent protein; RFP; plant; transgenic; GFP; Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana; Escherichia coli; green fluorescent protein; biotechnology.
                                                                       New DNA encoding red fluorescent protein, biotechnology, has sequence optimized for especially yeast or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2002
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                                                                                                                                                                                                            27-JAN-2000; 2000DE-02001395
                                                                                                                                                                                                                                        27-JAN-2000; 2000DE-02001395.
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                                                                                                                                                                                                                                                                                                  DE20001395-U1.
                                                                                                                                                                                                                                                                                                                               Anthozoa
                                                                                                                                                                               (GPCB-) GPC BIOTECH AG.
                                                                                                                                                 2002-228394/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                      optimised RFP
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                                                                                                                                ABA95905, ABA95921, ABA95922.
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ilarity 100.0%;
Conservative 0;
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                                                                                          expression
                                                                                                      useful as marker in
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The invention relates to DNA (I) containing either sequence ABA95905 sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein

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Disclosure;

Page 13-14; 19pp;

German.

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RESULT 5
AAE28833
ID AAE3
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Best Local S
Matches 225
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                                                                                                                                                                                                                                                                                                                                                                      Pluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; PRET; colouring agent; recombinant DNA application; analyte detection assausunscreen; second messenger detector; drFP583 protein; NFP-6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 225 AA;
                             New nucleic acid encoding a of an aggregating Cnidarian analyte detection assays or
                                                                                        WPI; 2002-691654/74.
N-PSDB; AAD46278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Discosoma
                                                                                                                                                                                                   21-FEB-2001;
04-DEC-2001;
                                                                                                                                                                                                                                                20-FEB-2002; 2002WO-US005749
                                                                                                                                                                                                                                                                               06-SEP-2002.
                                                                                                                                                                                                                                                                                                                                           Discosoma sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE28833 standard;
                                                                                                                                                                                                                                                                                                             WO200268459-A2
                                                                                                                                                                      (CLON-) CLONTECH LAB
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                   2001US-0270983P.
2001US-00006922.
                                                                                                                                         Lukyanov K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drFP583 (NFP-6) wild-type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                       INC.
                                                                                                                                         Yanushevich Y,
                              non-aggregating chromo- or fluorescent mutant
chromo- or fluorescent protein or mutant for
fluorescence activated cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No. 1e-127;
0; Mismatches 0
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Disclosure; Page 70-71; 80pp; English

The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) wild-type protein of the

Best Local Sim: Matches 225; Query Match Best Local (

Similarity

100.0%; Score 1214; DB 5; 100.0%; Pred. No. 1e-127; tive 0; Mismatches 0;

0;

0,

Gaps

Length Indels

Conservative

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Sequence 225

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RESULT 6
AAE17540
ID AAE17540
ID AAE17540
AC AAE1
XX AAE1
XX AAE1
XX Disc
XX Disc
XX Fluc
KW Prom
KW P
                                                                                                                                             New fluorescent timer proteins comprising an emission spectrum th changes over time from a first wavelength to a second wavelength, for monitoring intracellular protein movement, translocation, tra
                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fradkov
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                                Example 1; Fig 1; 89pp; English
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DB; AAD28207.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terskikh A;
                                                                                                                                                                                                         useful
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Fluorescent timer protein; protein movement; translocation; trafficking; promoter activity; gene expression; transgenic plant; gene modification; protein age; anthozoa protein; drPP583.

Discosoma sp. humanised wild-type Anthozoa protein drFP583.

22-APR-2002

(first entry)

AAE17540 standard; protein;

225

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RESULT 7
AAO18270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a fluorescent timer protein having an emission CC spectrum that changes over time after synthesis from a first wavelength CC to a second wavelength. The fluorescent timer proteins are useful in CC monitoring the activity of a promoter, determining the age of a protein, CC enriching a population of cells comprising a fluorescent timer protein. CC enriching a population of cells comprising a fluorescent timer protein. CC rive fluorescent timer proteins are also useful for assessing gene CC expression during development of a multicellular organism or during CC cellular differentiation, in response to a drug or other inducer of CC promoter activity, as a reporter to serve as a read-out of promoter activity, monitoring intracellular protein movement or translocation, CC protein trafficking, or protein stability, to investigate temporal CC visualisation of newly synthesised proteins and accumulated proteins, and CC visualisation of newly synthesised proteins and accumulated proteins, and ci distinguishing between newly formed and pre-existing structures, e.g. CC membrane junctions and extracellular matrix components. The fluorescent timer proteins and extracellular matrix components. The fluorescent componence in prokaryotic and eukaryotic cells, as selectable markers, as biosensors in prokaryotic and eukaryotic cells, in protease cleavage cassays, and as second messenger detectors. The nucleic acids can be used to assays, and as second messenger detectors. The nucleic acids can be used to generate transgenic, non-human plants or animals or site-specific gene modifications in cell lines. The present sequence is Discosoma sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 225 AA;
                 12-DEC-2000; 2000DE-01061872
                                                       12-DEC-2000; 2000DE-01061872.
                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                   Discosoma red fluorescent protein.
                                                                                                                                                                                                                                                                                                           26-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fluorescent
                                                                                                                                                                     Dівсовота вр.
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                                                                                                                                                                                                                               RAD54; promoter; genotoxicity cassette; cytotoxicity cassette;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                           yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMAKKPVOLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins
                                                                                                                                                                                                             strain; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1214; DB 5; 100.0%; Pred. No. 1e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                             pollution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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KVKPIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180

KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180

LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120

LSPQPQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY

120

MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60

MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI

60

181 181 121 121 61 61

YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225

YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225

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RRESULT 8
ADYS1716
ID ADYS
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a modified yeast strain that contains, integrated stably and functionally in its genome, a genotoxicity cassette and a cytotoxicity cassette, each comprising a promoter and reporter gene, both of which are different in the two cassettes. The modified yeast strain is used to detect environmental pollution, especially genotoxic and/or cytotoxic substances in complex environmental contaminants, especially organic compounds, but also (non-)ionising radiation and chemical carcinogens. Particular applications are in monitoring (waste) water (e.g. as an early warning system), medical toxicology screening and for industrial process control. The present sequence is a marker protein suitable for use in the cassettes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified yeast strain, useful to environment, contains integrated
                                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 21-22; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic compounds.
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                                                                                                                                                                                                                                                                                                                                                                     fluorescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADY51716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADY51716 standard; protein; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LICH/) LICHTENBERG-FRATE
                                                                                                                                                                                                                                                          WO200268605-A2
                                                                                                                                                                                                                                                                                                                  Discosoma
                                                        26-FEB-2001; 2001US-00794308.
24-MAY-2001; 2001US-00866538.
                                                                                                                                             26-FEB-2002; 2002WO-US006063.
                                                                                                                                                                                                     06-SEP-2002
     (REGC ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-539633/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVKFIGVNFPSDGPVMQKKIMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVBFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRSSKAVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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     CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                        mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                             wild type red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1214; DB 5
100.0%; Pred. No. 1e-127;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for detecting toxic compounds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
                                                                                                                                                                                                                                                                                                                                                                          red fluorescent protein; protein interaction
                                                                                                                                                                                                                                                                                                                                                                                                                             fluorescent protein (RFP) Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel non-oligomerizing fluorescent protein.

CC Specifically, it refers to the presence of at least one mutation in the CC fluorescent protein that reduces or eliminates the ability of the protein CC to oligomerize. The present invention describes fluorescent proteins CC derived from naturally occurring green or red fluorescent proteins and CC provides a fusion protein that comprises a non-oligomerizing fluorescent CC protein linked to at least one protein of interest. As such, these fusion CC proteins can be used in methods and compositions to determine the pH of a CC sample, or whether the sample contains an enzyme, molecule or agent that CC regulates the activity of an expression control sequence. Furthermore, CC they may be used to identify a specific interaction of molecules, such CC of molecular biology. This polypeptide sequence is the Discosoma sp. wild CC type red fluorescent protein (RFP) of the invention.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 225; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New non-oligomerizing fluorescent protein containing at least one mutation that reduces or eliminates the ability of the protein to oligomerize, useful for making better and new assays for molecular
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; SEQ ID NO 12; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-713372/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsien
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                                                                                                                                                                                LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVNNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHVTVKLKVTKGGPLPFAWDI
                                                                                                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
YMAKKPVQLPGYYYDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                               KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                       KVKFIGVNFPSDGPVMOKKTWGWEASTERLYPRDGVLKGBIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                       MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baird GS,
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                Score 1214; DB 5;
Pred. No. 1e-127;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zacharias
                                                                                                                                                                                                                                                                                                                                                             Length 225;
                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 9
AAE34962
ID AAE3
Phosphorylation indicator; fluorescent protein; kinase; red fluorescent protein; RFP.
                                                                                                                                      28-MAY-2003
                                                                                                                                                                          AAE34962 standard;
24-MAY-2001; 2001US-00865291
                  24-MAY-2002;
                                    28-NOV-2002
                                                                       Discosoma sp
                                                                                                                   Discosoma species red fluorescent protein (RFP)
                                                     WO200295058-A2
                  2002WO-US016955
                                                                                                                                      (first entry)
                                                                                                                                                                          protein; 225
                                                                                                                                                                            B
                                                                                                    detection; phosphatase;
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RESULT 10
ADC24126
ID ADC244
XX ADC24
XX D18C0
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Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or operative linkage, a donor molecule, a phosphorylatable domain, a phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Discosoma species red fluorescent protein (RFP) used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
                         26-FEB-2001;
24-MAY-2001;
                                                                                                             10-APR-2002; 2002US-00121258.
                                                                                                                                                                                                                       US2003059835-A1
                                                                                                                                                                                                                                                                              Discosoma
                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                     Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC24126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC24126 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 225
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                                                                                                                                                                                                                                                                                                                                                                 fluorescence
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                                                                                                                                                                                                                                                                                                                                                                                     Eluorescent
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                                                                                                                                                                                                                                                                                                                                 phosphatase; ion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wild-type red fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                           protein variant; transcription induction e energy resonance transfer; FRET; protein
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                         2001US-00794308.
2001US-00866538.
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100.0%; Pred. No. 1e-127;
tive 0; Mismatches C
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n kinase;
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The invention describes a polynucleotide sequence (I) encoding a CC Discosoma red fluorescent protein (DSRed) variant having a reduced compression amino acid substitutions at the AB CC and/or AC interfaces of the wild-type DSRed sequence (SI) comprising 225 cm in reduced propensity of the DSRed variant to form tetramers. (I) is CC useful for detecting transcriptional activity by providing a host cells conattining a vector which comprises (I) operatively linked to an CC expression control sequence, and an unit to assay the variant fluorescent protein fluorescence is indicative of transcriptional activity. A polynucleotide encoding a fusion protein is useful for the analysis of in vivo localisation or trafficking of a polypeptide of interest. A polypeptide marker is useful as markers to identify the location and amount of a ctarget protein produced, where the target protein and amount of a pollications involving fluorescence energy resonance transfer (FRET), which detects events as the function of the movement of fluorescent sensors for protein sinase and phosphatase activities or indicators for ions and molecules such as Ca2+, Zn2+, for identifying the protein of a first and second molecule, such as ca2+, Zn2+, for identifying the green for detecting induction of the marker, and control sequence of a molecule in a sample, for identifying a specific presence of a molecule in a sample, for identifying a specific contains an enzyme or for determining the ph of the sample. (I) is useful for identifying a region or condition that regulates the activity of an expression control sequence. This is the amino acid sequence of Discosoma wild-tyne red fluorescent protein or condition that regulates the activity of the protein protein
WPI; 2003-743764/70.
N-PSDB; ADC24127, ADC24134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1; 67pp; English.
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                                                        Discosoma wild-type red fluorescent protein.
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(CAMP/) CAMPBELL
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Sequence 225 AA;

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Best Local &
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                                                                                                                                                                                                                                         Similarity
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              YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                       KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                     KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGBIHKALKLKDGGHYLVEFKSI 180
                                                                                                              LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                     MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
YMAKKPYQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                             Conservative
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Pred. No. 1e-127;
; Mismatches 0;
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                                                                                                                                                                                                                                                       Length 225;
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RESULT 11 ABW00918

ABW00918

standard;

protein; 225

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RESULT 12
ADF70403
ID ADF70
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AC ADF70
XX
AC ADF70
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DT 12-FE
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Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a non-oligomerising fluorescent protein containing a mutation that reduces or eliminates its ability to oligomerise. The fluorescent protein gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH. These are also used to identify agents or conditions that regulate expression of control sequences. The present sequence is Discosoma sp. red fluorescent protein (RFP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Discosoma sp. red fluorescent protein (RFP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 30-31; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001US-00794308
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 225 AA;
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             12-FEB-2004
                                      ADF70403;
                                                               ADF70403 standard; protein; 225
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DB; AAD61969.
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ZACHARIAS D
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                                                                                                                                                   YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                       KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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                                                                                                                                MAKKPYQLPGYYYYDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                     KVKPIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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ilarity 100.0%;
Conservative 0
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Pred. No. 1e-127;
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                                                                                                                                                                                                                                                                                                                                                                           DB 7;
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RESULT 13
ADH34489
ID ADH34
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AC ADH34
XX
DT 11-MP
XX
DE Disce

ADH34489

standard;

protein;

Discosoma sp. 11-MAR-2004

(first entry)

red fluorescent protein DsRed (wild-type)

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Query Match
Best Local S
Matches 225
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23-JUL-2002;
11-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transformation of cells with a fusion protein of an orphan receptor protein with a fluorescent protein useful for identification of ligs to the orphan receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 26; 594pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-697654/66.
N-PSDB; ADF70404.
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                                                                                                                                                                                                                                                                                                               Similarity
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                      YMAKKPVQLPGYYYVDSKLDITSHWEDYTIVEQYERTEGRHHLFL
                                                                                                                       KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGBIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                     LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRIHLFL
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; 2002JP-00213949.
; 2002JP-00298237.
                                                                                                                                                                                                                                                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative (
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Pred. No. 1e-127;
0; Mismatches 0;
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CC (GFP)-like chromoproteins and fluorescent proteins exhibit some degree of CC homology, there are certain positions (referred to as 148, 165, 167 and CC 203; numbering corresponds to GFP) that are occupied by noticeably CC different residues in the two types of proteins. Mutagenesis of the CC residues in these key positions in, for example, a fluorescent protein, CC to those found in a chromoprotein is therefore proposed to confer CC chromoprotein activity on the fluorescent protein mutant, with CC chromoprotein being able to be converted into fluorescent proteins in a Similar manner. The invention also relates to expression constructs, vectors, host cells and host cell progeny comprising a nucleic acid of CC chromoprotein or fluorescent protein of an interconverted cc acid of CC chromoprotein or fluorescent protein of an interconverted cc interconverted mutant protein sof the invention. The interconverted cc interconverted mutant proteins of the invention. The interconverted cc compositions, pharmaceuticals, cosmetics and living organisms. Proteins activity can useful as colouring agents in, for example, food cc with chromoprotein activity are also useful as subscreens and selective filters. Chromoprotein CC untants having fluorescent protein and selective filters. Chromoprotein or CC compositions (e.g. the production of transgenic cells and organisms), and care also useful as sunscreens and selective filters. Chromoprotein CC untants having fluorescent protein applications, as biosensors in growaryotic and eukaryotic cells, as markers of whole cells to detect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived from a Cnidnarian species, preferably a non-bioluminescent
Cnidarian species, and most preferably an Anthozoan species. The
Chidarian is based on the finding that although green fluorecent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fluorescence resonance energy transfer; FRET; biosensor; whole cell marker; second messenger detector; in vivo marker; fluorescence activated cell sorting; fluorescent timer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to interconverted mutants of chromoproteins (CP) or fluorescent proteins (FP) and nucleic acids encoding them. The mutant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid encoding interconverted mutant of chromo-or escent protein which are useful as biosensors, coloring agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Fig 1; 56pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein activity. Con 197
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protein activity. Corresponds to GFP residue 165"
163
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protein activity. Corresponds to GFP residue 203"
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ponds to GFP residue 167"
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RESULT 14
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               messenger detectors, as in vivo markers in animals (e.g., transgenic animals), in fluorescence activated cell sorting applications, in protease cleavage assays, and in assays to determine the phospholipid composition in biological membranes. Proteins with fluorescent protein activity can also be used as fluorescent timers, where the switch of one fluorescent colour to another (e.g., green to red) is concomitant with the ageing of the protein and is useful for determination of the activation or deactivation of gene expression. The present sequence represents a wild-type red fluorescent protein, DaRed, from Discosoma sp. that was used as a parent sequence for the generation of mutant proteins in an example of the invention.
                                          New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, usefi in molecular biology, e.g. in immunoassays or in tracking protein
                              movement
                                                                                                       WPI; 2003-845265/78.
N-PSDB; ADL46204.
                                                                                                                                                                                                                                                          09-APR-2003; 2003WO-US010879
                                                                                                                                                                                                                                                                                                                                                    Discosoma sp.
                                                                                                                                                                                                                                                                                                                                                                                  oligomerization;
                                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma red fluorescent (DsRed) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL46203 standard;
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                                                                                                                                                                                                              10-APR-2002;
29-JUL-2002;
                                                                                                                                                                                                                                                                                                                        WO2003086446-A1
                                                                                                                                                                                                                                                                                                                                                                                               red fluorescent protein; DsRed; fluorescence;
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                              in cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRSSKNVIKBEMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AA;
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                                                                                                                                                   Campbell RE,
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                                                                                                                                                                                                              2002US-00121258
2002US-00209208
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  tetramerization; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                                                                                                      Baird
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                  red wavelength;
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                                                                                                                                                                                                                                                                                                                                                                                  hybridization
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                                                                                                                                                                                                                                                                                                                                                                                  assay
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                                                          useful
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Claim 1;

SEQ ID NO 1; 166pp;

English

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 225 AA;
                                                                                                                                                           Bevis B,
                                                                                                                                                                                                                            19-DEC-2001; 2001US-0341723P
                                                                                                                                                                                                                                                         18-DEC-2002; 2002WO-US040539
                                                                                                                                                                                                                                                                                                                         WO2003054158-A2
                                                                                                                                                                                                                                                                                                                                                           Discosoma
                                                                                                                                                                                                                                                                                                                                                                                          Cnidarian; fluorescence resonance energy transfer; FRET; wild-type DsRED
                                                                                                                                                                                                                                                                                                                                                                                                                          Wild-type DaRED protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN33979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN33979 standard;
             Claim 8; SEQ ID NO 2; 65pp; English.
                                             Novel nucleic acid encoding a rapidly maturing chromo- or fluoresc
mutant of a Cnidarian chromo- or fluorescent protein or its mutant
useful for applications involving chromo- or fluorescent proteins.
                                                                                                                                                                                            (UYCH-) UNIV CHICAGO
                                                                                                          2003-569236/53.
DB; ADN33978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%; Score 1214; DB 7; Similarity 100.0%; Pred. No. 1e-127; 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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                                                                                                                                                           Glick B;
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CC The present invention relates to nucleic acid that encodes a rapidly CC maturing chromo or fluorescent mutant of a Cnidarian chromo- or fluorescent protein or its mutant. The protein is useful in applications CC involving nucleic acid encoding a chromo- or fluorescent protein and is CC useful for producing a chromo and/or fluorescent protein which involves CC growing the cell, whereby the protein is expressed, and isolating the CC protein substantially free of other proteins. The protein and is useful as polying chromo- or fluorescent protein and is useful as CC primers, hybridization probes, etc. The expression cassettes are perful for synthesizing related proteins. The chromoproteins are useful as particular composition of matter e.g. food compositions cassettes are particular composition of matter e.g. food compositions, pharmaceuticals, CC cosmetics, living organisms, e.g., animals and plants. The chromoproteins for biological analytes of interest and as selectable markers in recombinant CC plants and proteins find use as labels in analyte detection assays, e.g. assays for the fluorescent proteins find use as electable markers in recombinant CC plants and proteins find use as a labels in analyte detection assays, e.g. assays for the automated screening of arrays of cells expressing fluorescence contains, as e.g. in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and enkaryotic cells, in applications involving the automated screening of arrays of cells expressing fluorescent proteins and in vivo marker in animals. The fluorescent proteins assays to determine the phospholipid composition in biological membranes and as a fluorescent timer. The present sequence represents the wild-rune nergy as a fluorescent timer. The present sequence represents the
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100.0%; Score 1214; DB 7; illarity 100.0%; Pred. No. 1e-127; Conservative 0; Mismatches 0;
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Result
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## ALIGNMENTS

	RESULT 1 JO1514
	green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)
	C;Species: Aequorea victoria C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
	C;Accession: JS0692; JQ1514; PQ0335; S48693; S51330; S51331 R;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.
	Gene 111, 229-233, 1992 A.Title: Primary structure of the Aequorea victoria green-fluorescent protein.
	A;Reference number: JQ1514; MUID:92175527; PMID:1347277
	A; Molecule type: DNA
	A;Residues: 1-107,'S',109-238 < KRAI> A.GROGET-OFGETENGE INTEROT: DATE: UNIPROT: 017105; UNIPROT: 017105; UNIPARC: UDIO00016B7F4
ש	A;CLUBE TELETANCES: VARIANCE TELETANCE A;CLUBE TELETANCE A;ACCEBBION JQ1114
rinted,	A; Molecule type: mRNA
	A; COOBE-references: UNIPARC: UPI0000002FB4; GB:M62653; NID:g155660; PIDN:AAA27721.1; PID:g
	A;Accession: PQ0335
	A; Modecuate type: provent A; Residues: 46-64;74-122;132-151;154-183;185-200 < PRA3>
on	A;Cross-references: UNIPARC:UPI0000173FD6; UNIPARC:UPI0000173FD7; UNIPARC:UPI000173FD8;
	R;Inouye, S.; Tsu]1, F.1.
rdiac mus	A. Tittle: Evidence for redox forms of the Aequorea green fluorescent protein.
rotein pr	A;Reference number: S48693; MUID:94364470; PMID:8082767
nding pro	A; Accession: \$48693
ptidase F	A; SCACUS: pretruitary
peptidylp	A, Residues: 1-24, 'Q', 26-156, 'P', 158-171, 'K', 173-238 < INO
membrane	A;Cross-references: UNIDARC:UP1000003582F; GB:L29345; NID:goob383; FIDN:AHABO240.1; FID:
ansducing	R;Watkins, J.N.; Campoell, A.N. submitted to the RMBL Data Library, January 1995
type prot	A; Reference number: \$51330
li adhesi	A;Accession: S51330
rotein -	A; MOLECULE Type: mx/M- A; Mol
cal prote	A;Cross-references: UNIPARC:UPI000007BC01; EMBL:X83959; NID:g634008; PIDN:CAA58789.1; PI
in 3 beta	A;Experimental source: Clone grp:
cal prote	A; Molecule type: mRNA
in synthe	A; Residues: 1-24, '0', 26-29, 'R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, '0', '155-170, '155-170, '155-170, 'B', '173-208, '0', '155-170, '155-170, 'B', '173-208, '0', '155-170, '15
prolyl iso	A;CIOSS-TETETENCES: UNIPARC:UPIUUUU/954U; ENDU:A0000V; ENTU:S000V; ENTU:S00V; ENTU:S00V; ENTU:S00V; ENTU:S00V; ENTU:S00V; ENTU:S00V; ENTU:S00V; ENTU:S00V; ENTU:S0
syndrome	RYANGE F. NOSS L.G.: Phillips Jr., G.N.
on enzyme	submitted to the Brookhaven Protein Data Bank, August 1996
-phosphat	A; Reference number: A65692; PDB:1GFL
rotein - h	A;Contents: annotation; x-ray Crystallography, 1.3 anystroums, restructs of 10 111.
oroly1 180	A; NOLE: ENGLINEELEG DESCRIPTION OF THE STATE OF THE STAT
abbit (fr	Nat. Biotechnol. 14, 1246-1251, 1996
EC 3.5.	$\mathtt{A}_i$ Title: The molecular structure of green fluorescent protein.

A; Title: The molecular structure of green fluorescent protein

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A;Molecule type: mRNA
A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>
A;Cross-references: UNIPARC:UPI000016B0B6; EMBL:X64699; NID:g37190;
                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI000016B0B9; EMBL:X83270; NID:g602579; PIDN:CAA58243.1; I A;Note: conformation and properties are reported for a synthetic peptide corresponding R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J. EMBO J. 11, 1711-1716, 1992
EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: $20897; MUID:92258380; PMID:1582406
A;Accession: $20898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 09-Jul-2004
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 09-Jul-2004
C;Accession: I38144; I83Quence revision 12-Aug-1996; S20899; S63665; S37393
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elast A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: I38344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q10466; UNIPARC:UPI000017CF2C; EMBL:X90568; NID:g1017424; R;Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A. Biochemistry 34, 553-561, 1995
Biochemistry 34, 553-561, 1995
A;Title: Dissecting titin into its structural motifs: identification of an alpha-helio A;Reference number: 138345; MUID:95119041; PMID:7819249
A;Accession: 138345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              titin, cardiac muscle [validated] - human N;Alternate names: connectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A58953; MUID:98294543; PMID:9631087
A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittir
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-
                                                                                                                                    A;Molecule type: mRNA
A;Residues: 13597-14200,'I',14202-14696 <LAB2>
A;Cross-references: UNIPARC:UPI00001680E7; EMBL:X64698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 몽
                                                                                                                        A;Accession: S20897
                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
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A;Residues: 1977-2014 <MUS>
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                                                                                         ;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PADIP--DYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT-GKLPVPMPTLVTTFSYGVQCFSRY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQYGSKVYVKH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDHMKQHDFFKSAMPEGYVQERTIFYKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG
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25.7%; Pred. No. 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation
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                                                                                                                                                    NID: g37192;
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      PIDN: CAA45940.1;
                                                                                                                                                       PIDN: CAA45939.1;
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A;Cross-references: UNIPARC:UP10000172573
R;Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, Fe
A;Reference number: A66736; PDB:ITIT
A;Contents: annotation; conformation by (1)H-NMR,
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A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the Brookhaven Protein Data Bank, August 1996 A;Reference number: A66201; PDB:1NCT
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A; Residues: 26831-26926 <GAU>
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A; Reference number: S37393; MUID:94008990;
A; Accession: S37393
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EMBO J. 12, 3827-3834, 1993
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A;Residues: 26729-26825 <KOL>
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21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,2484
;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental
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Best Local 9
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23726 RVIGSP 23731
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                                                                                                                185 KPVQLP 190
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                                                                                                                                                                                                                                                                                                                                            MOKKTMGWEASTERLYPRDGVLKGBIHKALKLK-----DGGHYLVEF------KSIYMAK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLAWSV--PEDEGGSKVTGYLIEMQKVDQHEWTKCNTTPTKIREYTLTHLPQGAEYRFRV 23610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAWDILSPQFQYGSKV--YV------KH-----PADIPDYKKLSFPEGFKWE-RV
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; Pred. No. 4.2e+02;
34; Mismatches 84;
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RESULT

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hap 90-binding protein p59 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A42386
R;Lebeau, M.C.; Massol, N.; Herrick, J.; Faber, L.E.; Renoir, J.M.; Radanyi,
J. Biol. Chem. 267, 4281-4284, 1992
J. Biol. Chem. 267, 4281-4284, 1992
A;Title: P59, an hap 90-binding protein. Cloning and sequencing of its cDNA
A;Reference number: A42386; MUID:92165768; PMID:1537818
A;Accession: A42386
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R;Shankar, V.; Baghdayan, A.S.; Huycke, M.M.; Lindahl, G.; Gilmore, Infect. Immun. 67, 193-200, 1999
A;Title: Infection-derived Enterococcus faecalis strains are enriche A;Title: Topic and the company of the com
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A42386
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C;Species: Enterococcus faecalis
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P27124; UNIPARC:UPI0000148548; G
A;Experimental source: liver
A;Experimental source: liver
A;Experimental source: liver
A;Experimental source: liver
C;Superfamily: human FK506-binding protein FKBP51; BKBP-type
C;Superfamily: human FK506-binding protein FKBP51; BKBP-type
F;50-97/Domain: BKBP-type peptidylprolyl isomerase homology
F;319-352/Domain: tetratricopeptide repeat homology <TT1>
F;353-386/Domain: tetratricopeptide repeat homology <TT2>
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A; Residues: 1-1873 <SHA>
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A;Accession: T30944
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:Q9Z4N7; UNIPARC:UPI00000B2A27; EMBL:AF034779; NID:g3873186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIP-DYKKLSPPEGPKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDG-PV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPOFQYGS------KVYVKHPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEGTSIESGTTVFAVKDGVSLP----EDKLPVLKAKDGYT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KSIYMAKKPYQLPGYYYVDSKLDITSHNEDYT 209
   FEVGEGESLDLPCGLEKAIQRMEKGEHSILYLKPSYAFGNAGKEKFQIPPY 240
                                                                                                                                                                                                                      EDGGVVTVTQDSSLQDGCFIYKVKFIGVNF--PSDGPVMQKKTMGWEASTERLYP----R
                                                                      DGVLKGE---
                                                                                                                                                                                                                                                                                                    AWDIAVATMKVGELCRITCKPEYAYGS---AGSPPKIPPNATLVFEVELFEFKGEDLTDD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.5%;
24.6%;
                                                                          ----IHKAL-KLKDGGHYLVEFKSIY----MAKKPVQLPGY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%; Score 92;
20.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  -----LSPQFQYGSKVYVKHPADIPDYKKLSFPE---GFKWERVMNF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Mismatches
                                                                                                                                                IRRIRTRGEGYARPNDGAIVEVALEGY - - YKDRLFDQRELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 91; DB 1; Length 458; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EGTSIESGTTVFAVK-DGVSLPEDKLPV 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YODGSVGTTDLAVTVSKNIYENPGE 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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<PPI>
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A;Notes: this sequence has been corrected
R;Masuda, E.S.; Anaguchi, H.; Sato, T.; Takeuchi, M.; Kobayashi, Y.
Nucleic Acids Res. 18, 657, 1990
A;Title: Nucleotide sequence of the sporulation gene spoIIGA from Bacill
A;Reference number: S08223; MUID:90174995; PMID:2106671
A;Reference number: S08223; MUID:90174995; PMID:2106671
A;Recession: S08223
A;Molecule type: DNA
A;Residues: 1410-1433 <MAS>
A;Cross-references: UNIPARC:UDI00016B97A; EMBL:X17344; NID:g40165; PID:
R;Kato, T.; Yamagata, Y.; Arai, T.; Ichishima, E.
Biogci. Biotechnol. Biochem. 56, 1166-1168, 1992
A;Title: Purification of a new extracellular 90-kDa serine proteinase w.
A;Reference number: JN0335; MUID:93005071; PMID:1368833
A;Accession: JN0335
A;Molecule type: protein
A;Residues: 195-218, 'A' <KAT'>
A;Residues: 195-218, 'A'
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A;Cross-references: UNIPARC:UPI0000172C26; GB:M29035
A;Note: the authors translated the codon GAA for residue 545
R;Wu, X.C.; Nathoo, S.; Pang, A.S.H.; Carne, T.; Wong, S.L.
J. Biol. Chem. 265, 6845-6850, 1990
A;Title: Cloning, genetic organization, and characterization
A;Reference number: A35750; MUID:90216713; PMID:2108961
A;Accession: A35750
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A;Residues: 1-392,'V', 394-828,'NIRTRLYSLKFCRSRHKSV' <WUA>
A;Residues: 1-392,'V', 394-828,'NIRTRLYSLKFCRSRHKSV' <WUA>
A;Residues: U-392,'V', 394-828,'NIRTRLYSLKFCRSRHKSV' <WUA>
A;Note: this sequence has been corrected
A;Note: this sequence has been corrected
A;Accession: B35750
A;Accession: B35750
A;Residues: B76-935,'CG' <WU2>
A;Residues: 876-935,'CG' <WU2>
A;Coss-references: UNIPARC:UPI0000B11CF; GB:J05400; NID:g142607; PIDN:AAA83363.1;
A;Cross-references: UNIPARC:UPI0000B11CF; GB:J05400; NID:g142607; PIDN:AAA83363.1;
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J. Bacteriol. 172, 1470-1477, 1990
J. Fittle: Bacillopeptidase F of Bacillus subtilis: purification of the protein and c A;Reference number: A35131; MUID:90170864; PMID:2106512
A;Accession: A35131
A;Cross-references: UNIPARC: UPI000016E868; GB:M22630; NID:g142938; PIDN:AAA22458.1; PID:gR;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterg, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallergiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
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A; Residues: 1-211 < RES>
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RESULT 6
B70476
hypothetical protein aq 2054 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70476
C:Accession: P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gra
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C;Superfamily: bacillopeptidase F; subtilisin homology
C;Keywords: extracellular protein, hydrolase; serine proteinase
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-194/Domain: propeptide #status predicted <PRO>
F;195-1433/Product: bacillopeptidase F #status experimental <MA?
F;218-466/Domain: subtilisin homology <SBT>
F;227,274,452/Active site: Asp, His, Ser #status predicted
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A;Residues: 1-116 <AQF>
A;Cross-references: UNIFROT:067838; UNIFARC:UPI00000567A2; GB:AE000770; NID:g2984274;
A;Cross-references: Btrain VF5
                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70476
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A; Cross-references: UNIPARC: UPI0000060385;
A; Cross-references: Strain 168
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A;Accession: B69596
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KDLLLDSEYFSAKTKGEIKRNTGEILAEVEIKEIRKENFTLSGTKINAKGTINLPVLDIN
                                            KNVIKEFMRFKVRMEGTVNGHEFEIEGEGE------
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                                                                                             7.2%; Score 87.5; [larity 22.0%; Pred. No. 21; Conservative 35; Mismatches
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; Pred. No. 21;
26; Mismatches
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C;Accession: ...
R;Brieman, A.
submitted to the EMBL Data
submitted to number: Z15713
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A;Cross-references: UNIPROT:004843;
A;Experimental source: cv. ATIR, 2 <
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169-212/Domain: BKBP-type peptidylprolyl isomerase homology cPPI2>
169-212/Domain: BKBP-type peptidylprolyl isomerase homology cPPI2>
186-334/Domain: BKBP-type peptidylprolyl isomerase homology cPPII>
188-334/Domain: BKBP-type peptidylprolyl isomerase homology cPPII>
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AVPPNSTLHIDLQLVSWKTLTLIGDDKRILKKVLKEGEGYER
                                                                                  YYYVDSKLDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K-GWDQGIKTMKKGENASLTIPPDLAYGERA----PRTIPPNATLRFDVELLSWASVKDI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKLVKEGEGWDTAETALKVEVHYTGTLLDGTKFD-SSRDRGTPF-----KFKLEQGQVI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNVIKE-----FMRFKVRMEGT-VNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVFQDFNAYLSGEGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFENLVVDKNTLGINREIRGEFHGNGKVDFKKMFVKVN-----
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                                                                                                                                                                                                                                      QKKTMGWEASTERLYPRDGVLKGEIHKALK-LKDGGHYLVEFKSIY----MAKKPVQLPG 191
                                                                                                                                                                                                                                                                                                                    CKDGGIFKKVLVEGQKWE---NPKDLDEVTVKYEARLEDGSVVSKSESI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVEQ----YERTEGR 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                   ----KDGYFCPALSKAVKTMKKGEKVLLTVKPQYGFGEQGRAATEVEG
                                                                                                                                                                                                                                                                                                                                                                                              EGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library,
                                                                         -----EQYER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 87; DB 2;
Pred. No. 9.3;
2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; UNIPARC:UPI00000AD075; El day old plants, root tips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   August
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: Y07636; PIDN: CAA68913.1
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probable membrane protein [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 0: C;Accession: C97196

#text\_change 09-Jul-2004

RESULT C97196

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eignal-transducing histidine kinase homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69397
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A;Accession: G69397
A;Accession: G69397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1484 «KUR»
A;Residues: 1-1484 «KUR»
A;Cross-references: UNIPROT:Q97GG4; UNIPARC:UPI00000CA4ED; GB:AE001437; PIDN:AAK80358.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97196
A;Status: preliminary
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A; Residues: 1-456 < KLE>
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Best Local 9
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                                                                                                                                                                                                                                                                 y Match 7.0%; Score 85.5; DB 2; Length 456;
Local Similarity 22.0%; Pred. No. 9.5;
hes 46; Conservative 25; Mismatches 59; Indels 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKKPVQLPGYYYVDS-----KLD------ITSHNEDYTIVEQYERTEGRHHLF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VK--KAETAKVYIR-----ALVSKSGGKLKVTVGKKSVYVDTFDESKSQFKWIYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEFMRFKVRMEG-----TVNGHEFEIEG-----BGEGRPYEGHNTVKLKVTKGGP 53
                                                                                                                                                                                                                EFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQYGSKVYVKHPADIPDYKKL
                                                                                                                 SFPEGFKWERVMNFEDGGVVTVTQDS-----SLQDGCFIY------KVKFIGVN
                                                                                                                                                                  EFEELGE-EGRFYESR-----YITKDGRVRHVWGFTAKFTFLGKSYIIGNWIDVTKSKEL 120
                                                                  -----EQALRESEEFYRTLVEDSLTPVYLLQDGIMVYVNKAFEEATGYKREEIVGRN 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 87;
Pred. No.
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. 33,
                       TMGWEASTERLYPRDGVLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
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                                                                                                                                                                                                                                                                      79;
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                                                                                                                                                                                                                                                                                                                  G.; Weissenbach, J.; Petit, C
Cell 67, 423-435, 1991
A;Title: The candidate gene for
A;Reference number: A40351; MUI
A;Accession: A40351
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-679 <LEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein AF1543 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69442
R;KLenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Clodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adhesion-type protein ADMLX - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Mar-2004 C;Accession: A40351 R;Legouis, R.; Hardelin, J.P.; Levilliers, J.; Claverie, J.M.; Compain, S.; G.; Weissenbach, J.; Petit, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-271 < KLE>
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                         S
                                                                                                                                                                       A;Gene: GDB:KAL1; KAL
A;Cross-references: GDB:120116; OMIM:308700
A;Map position: xp22.32-xp22.32
F;129-175/Domain: antileukoproteinase repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI000016B3D2; GB:S60085; NID:g237595; PIDN:AAB20108.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                          Matches
                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watch 7.0%; Score 85; DB 2; Length 271; Local Similarity 25.6%; Pred. No. 5.2; 1es 44; Conservative 18; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
  46 LKVTKGG---PLPF---
                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRD-----GVLKGEIHKALK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFFLIHPEDRGLVYKRYIEREKGLRDTMETYSW-----RIIRKDGEVRWVTARPGRVTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDA---YMISTLLHLYNRDVPEETKMLV-----RRYRRETEFGVGYGVKKPNLEETFY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFQYGSKVYVKHP-----ADIPDYKK--LSFPEGFKWERVMNFEDGGVV---TVTQDSSL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ASYILRDKAVISFVKSFESNGGFAKQPGGYPPYLEDTYYATSTLSLLS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKDGGHYLVEFKSIY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTBINSLFYTLHSLNLLGEDLPDYSSFLLKRLEGLKAERKYLLSDGGVTATYTFLQPNAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- GEIHKA-LKLKDGGHYL 174
                                                                                                 7.0%; Score 84.5;
27.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                         for the X-linked Kallmann syndrome MUID:92005720; PMID:1913827
---AMDILSPQFQYGS---KVYVKHPAD--IPDYKKLSFPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --MAKKPVQLPGY----YYVDSKLDITS 203
                                                                                                                                踞
                                                                                                                           2
                                                                               75;
                                                                                                                           Length 679;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.M.; Compain, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wunderle,
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C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane F;1-19/Domain: signal sequence #status predicted <SIG> F;34-98/Domain: immunoglobulin homology <IMM1> F;33-191/Domain: immunoglobulin homology <IMM2> F;132-191/Domain: immunoglobulin homology <IMM2> F;152-156/Region: heparin binding #status predicted F;161-165/Region: heparin binding #status predicted F;161-165/Region: heparin binding #status predicted F;263-290/Domain: immunoglobulin homology <IMM3> F;263-272/Region: NCAM binding #status predicted F;323-388/Domain: immunoglobulin homology <IMM4> F;420-482/Domain: immunoglobulin homology <IMM5> F;420-482/Domain: immunoglobulin homology <IMM6> F;420-482/Domain: immunoglobulin homology <I
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A;Molecule type: DNA
A;Residues: 642-656,'D',658-725 <BA2>
A;Rougon, G.; Marshak, D.R.

1. Blol. Chem. 261, 3396-3401, 1986
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Reference number: A44290; MUID:86140120; PMID:3512556
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R;Barthels, D.; Santoni,
EMBO J. 6, 907-914, 1987
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C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type:
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A;Residues: 1-725 <BAR>
A;Cross-references: UNIPROT:P13594; UNIPARC:UPI0000028AC3;
D:Rarbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
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A; Introns: 701/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neural cell adhesion molecule 1 precursor,
                                                                                                                                                                                                                                                                                                                                                                                                             ;519-596/Domain: fibronectin type III repeat homology <FN3A>;625-685/Domain: fibronectin type III repeat homology <FN3B>,625-685/Domain: fibronectin type III repeat homology <FN3B>,305-386,330-386,427-480/Disulfide bonds: #Breatus predicted;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #Breatus predicted;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #sta
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;Accession: A29673; S00382; Ā44290
;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;420-482/Domain:
;519-596/Domain:
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                                                                                                                                                                                                                                                    Matches
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            148
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                                                                                                                                                                                                                                                                                             Similarity
        ERLYPRDGVLKGEIHK-----ALKLKDGG----HYLVEFKSIYMAKKP-VQLP-GYY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFTTPPCSALKGKSHKPIGCLGEAGHVLSK-----VLAKPENLSASFIVQD-VNITGH 567
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                                                                                           FTWYDAKEANMEGIVTIMGLKPETTYSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y---PRDGVLKGEIHKALK-LKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSKLDITSH 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAHNRTTGSEASSGMTHENYIILQDLSFSCKYKV-----TVQPIRPKS----HSKAEAV 515
                                                                                                                                                                     FKWERVMNFEDGGVVTV---TQDSSLQDGCFIYKVKFIGVNFPSDGFVMQKKIMGWEAST 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTERL 150
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                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                             24.2%;
                                                                                                                                                                                                                                                                                         7.0%; Score 84.5; DB 1;
24.2%; Pred. No. 21;
                                                                                                                                                                                                                                                        30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPI-anchored splice
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                                                                                               -RLAALNGKGLGEIMQPSESKTQPVP
                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                                                                   Length 725;
                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL:Y00051; NID:g53342; PID
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R;Aubert-Pivert, E.; Davies, J.

Gene 147, 1-11, 1994

A;Title: Biosynthesis of butirosin in Bacillus circulans
A;Reference number: Z18808; MUID:94374689; PMID:7522196
A;Accession: T17884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: butB
C;Function:
A;Pathway: butirosin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1616 < AUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:P35824; UNIPARC:UPI0000135A00; EMBL:L20421; NID:g304142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T17884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Species: Bacillus circulans;
Date: 15-Oct-1999 #sequence_revision;
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Best Local
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                                                                                                                                       KSFTSEVRQLTDR---VKAEKGKKIEVSAYVGSWFESYYLNGVHWGSTEFRYDERLRMKD 809
                                                                                                                                                                          MGWEASTERLYPRDGVLKGEIHKALKLK------DGGHY-LVEFK---SIYMAK 184
                                                                                                                                                                                                                      RYDNESADFSDLTKAKFESFLGARGKOLONWPDDVFTYAGNVRKDGPLIRDWWEFRSKTI 752
                                                                                                                                                                                                                                                           TQDSSLQDGCFIYKVK---FIGV-----NFP-----SDGPVMQ-----KKT 140
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                                                                                                                                                                                                                                                                                                                                     GGPLPFAWDILSPQFQYGSKVYVKHPAD-IPDYKKLSFPEGFKWERVMNFEDGGVV--TV 107
                                                             KSVYTPGYYESGYV------KNLDFIMIGAYQTTAPEIEHYITL
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Pred. No.
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conserved hypothetical protein [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Pate: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004 C;Accession: E90276 R.K.; Confalonieri, F.; Zivanovic. Y.: Allard G. Amanana, R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic. Y.: Allard G. Amanana, R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic. R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Tlarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome. A;Cross-references: UNIPROT:Q97YT6; C;Genetics: A; Molecule type: DNA A; Residues: 1-268 < KUR> A, Status: preliminary A; Accession: E90276 A; Reference number: A99139 UNIPARC: UPI00000643B4; GB: AE006641; X.; Thi-Ngoc, G.; Awayez, M.J.; Chan-V hi-Ngoc, H.P.; Redder, P. NID: 913814420;

2

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RESULT 15

E89544

E89544

hypothetical protein AF2357 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: E69544
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A;Attle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Atterns: preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: E69544
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A;Residues: 1-340 <KLE>
A;Cross-references: UNIPROT:O30313; UNIPARC:UPI00000572DC; GB:AE001113; GB:AE000782; NII
Search completed: January 11, 2006, 02:04:50 Job time : 18 secs
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les 38; Conserv
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                                                                                                                                       251
                                                                                                                                                                                                                                                                              193 -SRVVTVLPNGSVLDLTSNY-TKTYNVTITIDONVEKGILKVTTWKGSVERTVYSKAVNK 250
                                                                                                                                                                                                                                                                                                                                           101 DGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQ--KKTMGWEASTERLYPRDGVLK 158
                                                                                                                                                                                                                                                                                                                                                                                                               144 HAWVEVKINN-----SWVVADPTVYW---LYVNYPEKYPNWNKLWP-NNESWANLIDF- 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        '41 HNTVKLKVTKGGPLPFAMDILSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFE 100
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                                                                                                                                                                                  GB-IHKALKLKDGGHYLVBFKSIYMAKKPVQLPGYYYVD 196
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2: uniprot_trembl:*
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Discosomatidae; D NCBI\_TaxID=86600; [1] NUCLEOTIDE SEQUENCE.
MEDLINE=99436614; Pubmed=10504696; DOI=10.1038/13657;
MATZ M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., PubMed=11101896; DOI=10.1038/81992; Wall M.A., Socolich M., Ranganathan R.; "Fluorescent proteins from nonbioluminescent Anthozoa species."; Nat. Biotechnol. 17:969-973(1999). -"The structural basis for red fluorescence in the tetrameric homolog DsRed.",  $\label{eq:constraints}$ Markelov M.L., K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). BIOPHYSICOCHEMICAL Absorption: Struct. Biol. Abs (max) =558 nm; Lukyanov S.A.; Discosoma. 7:1133-1138(2000). PROPERTIES: GFP

<del>-</del>

SUBUNIT: Homotetramer.

PTM: Contains a chromophore consisting of modified amino acid residues. The chromophore is formed by autocatalytic backbone residues. The chromophore is formed by autocatalytic backbone condensation between Xaa-N and Gly-(N+2), oxidation of Tyr-(N+1) to didehydrotyrosine, and formation of a double bond to the alphanon nitrogen of residue Xaa-N. Maturation of the chromophore requires nothing other than molecular oxygen.

BIOTECHNOLOGY: Fluorescent proteins have become a useful and ubiquitous tool for making chimeric proteins, where they function ubiquitous tool for making chimeric proteins, where they function as a fluorescent protein tag. Typically they tolerate N- and C-

Note=Exhibits a smaller absorbance peak fluorescence emission spectrum peaks at

at 494 nm. 583 nm;

The broad

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QGENDT QGENDT ID NO QGENDT 255 DT 255
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PDB; 1G7K; X-ray; A/B/C/D=2-225.

PDB; 1GGX; X-ray; A/B/C/D=1-225.

InterPro; IPR011584; GFP_related.

InterPro; IPR000786; Green_fl_protein.

Pfam; PF01353; GFP; 1.

PRINTS; PR01229; GFPLUORESCENT.

PRODOM; PD013756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence up
25-OCT-2004 (TrEMBLrel. 28, Last annotation
Enhanced red fluorescent protein R+.
Discosoma sp. RC-2004.
Eukaryota; Metazoa; Chidaria; Anthozoa; Zoan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD013756; Green_fl_protein; 1.
3D-structure; Chromophore; Luminescene; Photoprotein.
MOD_RF.3
67 67 (2)-2,3-didehydrotyrosine.
CROSILNK
66 68 2-iminomethyl-5-imidazolinone (Gln-Gly).
SEQUENCE 225 AA; 25931 MW; FBF9A5369778F689 CRC64;
                                                                                          NUCLEOTIDE SEQUENCE.

Carter R.W., Gibbs P.D.L., Schmale M.C.;

Carter R.W., Gibbs P.D.L., Schmale M.C.;

"Cloning of Anthozoan Fluorescent Protein Genes.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AY679107; AAU04444.1; -; mRNA.

GO; GO:0006091; P:generation of precursor metabolites an InterPro; IPR011384; GFP related.

InterPro; IPR010786; Green_fl_protein.

Pfam; PP01353; GFP; 1.
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NCBI_TaxID=289055;
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            PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein;
SEQUENCE 236 AA; 27032 MW; BB38
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hes 225;
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SIMILARITY: Belongs to the GFP family.
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Similarity 100.0%; Pred. No. 1e-96;
25; Conservative 0; Mismatches 0; Indels
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in no way modified and this
                  BB3844BE06829EF0 CRC64;
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Wiedenmann J., Girod A.;

Wiedenmann (SEP-2002) to the EME
Submitted (SEP-2002) to the EME
EMBL; AF545888; AAQ11987.1; -;

HSSP; P42212; 1B9C.
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                                                                                                                                                                                                                                                                                                    ProDom; I
                                                                                                                                                                                                                                                                                                                                   GO; GO:0006091; P:generation of precus
InterPro; IPR0011584; GFP related.
InterPro; IPR0007966; Green fl protein.
Pfam; PF01353; GFP; 1.
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Q6KF85;
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Discosomatidae; Discosoma.
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PD013756; Green_fl_protein; 1.
E 225 AA; 25791 MW; E151D0E497AA23FA CRC64;
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"Cloning of Anthozoan Fluorescent Protein Genes."
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ dai
EMBL; AY679106; AAU04443.1; -; mRNA.
GO; GO:0006091; P:generation of precursor metabol
InterPro; IPR011584; GFP_related.
InterPro; IPR001584; GFP_related.
InterPro; IPR00786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PF01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 236 AA; 27042 MW; BB3844BCD6834EF3
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Discosoma sp. RC-2004.
Eukaryota, Metazoa; Cnidaria;
Discosomatidae; Discosoma.
NCBI_TaxID=289055;
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                                                            EMBL; AF272711; AAG16224.1; -; mRNA.
HSSP; Q9U6Y8; 1GGX.
GO; GO:0006091; P:generation of precursor |
InterPro; IPR011584; GFP_related.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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MEDLINE-20434599; PubMed-10981720; DOI-10.1016/S0014-5793(00)01895-0;
Fradkov A.F., Chen Y., Ding L., Barsova E.V., Matz M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Discosoma sp. SSAL-2000.
Eukaryota; Metazoa; Cnidaria;
Discosomatidae; Discosoma.
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                                                                                                                                                                                                                                                         "Novel fluorescent protein from Discosoma possesses a unique far-red fluorescence.", FEBS Lett. 479:127-130(2000).
                                 PRINTS;
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PubMed=15556995; DOI=10.1073/pnas.0407752101;

Wang L., Jackson W.C., Steinbach P.A., Tsien R.Y.;

Wang L., Jackson W.C., Steinbach P.A., Tsien R.Y.;

Wang L., Jackson W.C., Steinbach P.A., Tsien R.Y.;

"Evolution of new nonantibody proteins via iterative son hypermutation.";

Proc. Natl. Acad. Sci. U.S.A. 101:16745-16749(2004).

EMBL; AY786536; AAV65486.1; -; mRNA.

GO; GO:0006091; P:generation of precursor metabolites and InterPro; IPR001584; GFP_related.

InterPro; IPR001788; Green_fl_protein.
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Discosoma sp. LW-2004.
Eukaryota, Metazoa, Chidaria, Anthozoa,
Discosomatidae, Discosoma.
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
PRODOM; PD013756; Green fl protein; 1.
SEQUENCE 226 AA; 25513 MW; 159A8FBE2D453A5B CRC64;
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RESULT 7 Q583G7\_9CNID ID Q583G7\_9CNID

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                                                                                                                      "Survey of coral GFP-like proteins";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ
EMBL; AY646074; AAU06853.1; -; mRNA.
GO; GO:0006091; P:generation of precursor meta
InterPro; IPR011584; GFP_related.
InterPro; IPR011584; GFPenfl_protein.
Pfam; PF01353; GFP; 1.
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Eukaryota; Metazoa; Cnidaria; Anthozoa; 2
Astrocoeniina; Acroporidae; Acropora.
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Discosoma sp. LW-2004.
Eukaryota; Metazoa; Chidaria;
Discosomatidae; Discosoma.
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Alieva N.O., Meleshkevitch E.A.,
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InterPro; IPR011584; GFP related.
InterPro; IPR001786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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                                 PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein;
SEQUENCE 221 AA; 25103 MW; 3BEA
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PD013756; Green fl_protein; 1.
E 226 AA; 25530 MW; 6DF38CADZAB28BED
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"Survey of coral GFP-like proteins.";
Submitted (JUN-2004) to the EmBL/GenBank/DDBJ dat
EMBL; AY646077; AAU06856.1; -; mRNA.
GO; GO:0006091; P:generation of precursor metabo.
InterPro; IPR0011584; GFP_related.
InterPro; IPR0011584; GFP_related.
InterPro; IPR001786; Green_fl_protein.
Ffam; pF01353; GFP; 1.
PF1NTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 221 AA; 24976 MW; 307DE4FC4B018B43
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Astrocoeniina; Acroporidae; Acropora.
NCBI_TaxID=287157;
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Pred. No. 8.9e-61;
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Eukaryota; Metazoa; Cnidaria; Anthozoa;
Astrocoeniina, Acroporidae; Acropora.
                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE, SUBUNIT, AND MUTAGENESIS OF ASN-142.
MEDLINE-2153626; PubMed=11682051; DOI-10.1016/S0014-5793(01)02930-1;
Gurskaya N.G., Fradkov A.F., Terskikh A., Matz M.V., Labas Y.A.,
Martynov V.I., Yanushevich Y.G., Lukyanov K.A., Lukyanov S.A.;
"GFP-11ke chromoproteins as a source of far-red fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goniopora tenuidens (Coral).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
Fungiina; Poritidae; Goniopora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1229; GFLUORESCENT.
PRODOM; PD013756; Green_fl_protein; 1.
SEQUENCE 221 AA; 24987 MW; 546D2CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Survey of coral GFP-like proteins.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY646075; AAU06854.1; -; mRNA.
GO; GO:0006091; P:generation of precursor metabolites an
InterPro; IPR011584; GFP_related.
InterPro; IPR010786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFP-like non-fluorescent chromoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2005 (Rel. 46, Created)
01-FEB-2005 (Rel. 46, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q95P04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GONTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF01353; GFP; 1
                                                                                                                                                                                                                     3 Lett. 507:16-20(4001).
FUNCTION: Non-fluorescent pigment
BIOPHYSICOCHEMICAL PROPERTIES:
PTM: Contains a chromophore consisting of modified amino acid residues. The chromophore is formed by autocatalytic backbone condensation between xaa-N and Gly-(N+2), oxidation of Tyr-(N+1) to didehydrotyrosine, and formation of a double bond to the all amino nitrogen of residue xaa-N. Maturation of the chromophore requires nothing other than molecular oxygen. The precise
                                                                                                                                                           SUBUNIT: Homotetramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _TaxID=75301;
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                                                                                                                                                                                                             Absorption:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
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Pred. No. 1.1e-60;
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25-OCT-2004 25-OCT-2004 25-OCT-2004

(TrEMBLrel. 28, (TrEMBLrel. 28, (TrEMBLrel. 28,

Last Last

sequence up

update) update)

Chromoprotein

Acropora hyacinthus.

Q66PU9\_9CNID

PRELIMINARY;

PRT;

221

8

9CNID

Eukaryota; Metazoa; Cnidari Astrocoeniina; Acroporidae;

Cnidaria;

Anthozoa;

Zoantharia; Scleractinia;

NCBI\_TaxID=55974;

"Survey of Alieva N.O., NUCLEOTIDE

(JUN-2004)

., Meleshkevitch E.A., coral GFP-like protei

EMBL/GenBank/DDBJ

S.F.,

Matz M.V.;

SEQUENCE

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MOD_RES
CROSSLNK
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
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GO; GO:0010117; P:photoprotection; ISS
InterPro; IPR011584; GFP_related.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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-!- SIMILARITY: Belongs to the GFP family.
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63 63 2,3-didehyd
62 64 2-iminomerh
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N->S: Produces a f:
; 93F9F4B5C2003CB4
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Pred. No. 2.4e-60;
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2-iminomethyl-5-imidazolinone (Gln-Gly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                          nonplanar chromophore conformation.";

Structure 11:275-284 (2003).

-I- FUNCTION: Thought to play a role in photoprotection resident symbiont microalgae's photosystems from photosystems by high light levels found near the surface caused by high light levels found near the surface c-i- SUBUNIT: Homotetramer.

-I- PTM: Contains a chromophore consisting of modified a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2005 (Rel. 46, Created)
01-FEB-2005 (Rel. 46, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
GFP-like non-fluorescent chromoprotein (Rtms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AY646076; AAU06855.1; -; mRNA.
GO; GO:0006091; P:generation of precursor metabor interpro; IPR011584; GFP related.
Interpro; IPR010786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 221 AA; 24963 MW; FC9D9E749069D079
                                                                                                                                                                                                                                                  MEDLINE=22511991; PubMed=12623015; DOI=10.1016/S0969-2126(03)00028-5; Prescott M., Ling M., Beddoe T., Oakley A.J., Dove S., Hoegh-Gulüberg O., Devenish R.J., Rossjohn J.; "The 2.2 A crystal structure of a pocilloporin pigment reveals a
                                                                                                                                                                                                                                                                                                                                                                                                           CRYSTALLIZATION.
PubMed=12595737; DOI=1
Beddoe T., Ling M., Dc
Prescott M., Rossjohn
                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 HIS-142 AND PHE-158. MEDLINE=22511991; PubMed=12
                                                                                                                                                                                                                                                                                                                                                               "The production, purification and crystallization pigment from a reef-forming coral."; Acta Crystallogr. D 59:597-599(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pocilloporin).
Montipora efflorescens (Coral).
Eukaryota, Metazoa, Chidaria, Anthozoa,
Astrocoeniina, Acroporidae, Montipora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFCP_MONEF
P83690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=105610;
           PTM: Contains a chromophore consisting of modified amino residues. The chromophore is formed by autocatalytic back condensation between Xaa-N and Gly-(N+2), oxidation of Ty to didahydrotyrosine, and formation of a double bond to t amino nitrogen of residue Xaa-N. Maturation of the chromo requires nothing other than molecular oxygen. BIOTECHNOLOGY: Fluorescent proteins have become a useful ubiquitous tool for making chimeric proteins, where they as a fluorescent protein tag. Typically they tolerate N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          DOI=10.1107/S0907444902023466;
 င်
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                                                                                                                                                                                                                                                                                                                                 ANGSTROMS), SUBUNIT,
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DRRTA PROCESS OF THE 
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Best Local &
Carter R.W., Gibbs P.D.L., Schmale M.C.; "Cloning of Cnidarian Fluorescent Protein Genes."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ database EMBL; AX679108; AAU04445.1; -; mRNA.

GO; GO:0006091; P:generation of precursor metabolites InterPro; IPR011584; GFP_related.
                                                                                                                                                                                                            Discosoma striata (Striped mushroom).
Eukaryota; Metazoa; Chidaria; Anthozoa;
Discosomatidae; Discosoma.
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MUTAGEN
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PDB; 1MOV; X-ray; A=3-221.
GO; GO:0018995; C:host; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=105400;
                                                                                                                                                                                                                                                                             Cyan fluorescent protein C1.
                                                                                                                                                                                                                                                                                                                                                                                          Q66ND6_DISST PRELIMINARY;
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InterPro; IPR011584; GFP_related.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Q66ND6;
25-OCT-2004
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MISCELLANEOUS: The wild-type form is non-fluorescent with the color being pH dependent, ranging from yellow at low pH, through the color being pH dependent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
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221 AA;
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63 63
62 64
142 142
158 158
21 AA; 24911 M
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(E)-2,3-didehydrotyrosine.
2-iminomethyl-5-imidazolinone
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                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 782; DB 1;
Pred. No. 2.1e-59;
3; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H->S: Produces a fluorescent F->H: Produces a homodimeric
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                                                                                                                                                                                                                                       Zoantharia;
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                              energy;
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Q9U6Y7;
                                             -I- PTM: Contains a chromophore is formed by autocatalytic backbone residues. The chromophore is formed by autocatalytic backbone condensation between Xaa-N and Gly-(N+2), oxidation of Tyr (N+1) to didehydrotyrosine, and formation of a double bond to the alphanamino nitrogen of residue Xaa-N. Maturation of the chromophore requires nothing other than molecular oxygen. The precise stereochemistry of the tyrosine has not been determined.

-I- BIOTECHNOLOGY: Fluorescent proteins have become a useful and ubiquitous tool for making chimeric proteins, where they function as a fluorescent protein tag. Typically they tolerate N- and C-terminal fusion to a broad variety of proteins. They have been expressed in most known cell types and are used as a noninvasive fluorescent marker in living cells and organisms. They enable a wide range of applications where they have been expression, protein interactions.

-I- SIMILARITY: Belongs to the GFP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2005 (Rel. 46, Created)
01-FEB-2005 (Rel. 46, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
GFP-like fluorescent chromoprotein dsFP483.
Discosoma striata (Striped mushroom).
Bukaryota, Metazoa, Chidaria, Anthozoa, Zoantharia; Corallimorpharia;
Discosomatidae, Discosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 227 AA; 25640 MW; 5686393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY.
MEDLINE-99436614; PubMed=10504696; DOI=10.1038/13657;
MEDLINE-99436614; PubMed=10504696; DOI=10.1038/13657;
MEL, J., Labase Y.A., Savitsky A.P., Zaraisky A.G.,
Markelov M.L., Lukyanov S.A.;
"Fluorescent proteins from nonbioluminescent Anthozoa species.";
Nat. Biotechnol. 17:969-973(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=105400;
                  Thie
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Pigment protein that BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Oral disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Absorption:
Swiss-Prot entry is copyright. It is produced through a collaboration - een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                         Abe(max)=443 nm;
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HSSP; Q9U6Y8; 1GGX.
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133; Conserv
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PRO1229; GFLUORESCENT.

PRO13756; Green fl proteprotein.

phore; Luminescence; Photoprotein.

2,3-didehydrotyrosine (By similarity).

S 67 67 2,3-didehydrotyrosine (Gin-Gly)

NK 66 68 (By similarity).

NK 66 68 (By similarity).

AA8F18EEE283CE4D CRC64;
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8; Mismatches 53
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5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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Copyright (c) 1993 - 2006 Compugen Ltd
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US-09-866-538-12
US-09-865-291-12
US-10-152-296-2
US-10-122-296-2
US-10-244-779-2
US-10-244-779-2
US-09-277-716-16
US-09-626-581D-65
US-09-626-580C-65
US-09-971-897-13
US-09-977-897-13
US-09-977-897-16
US-09-977-897-17
US-09-977-897-18
US-09-977-897-19
US-09-977-897-19
US-09-977-897-19
US-09-977-897-19
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e 12, Apple 2, Appli e 2, Appli e 2, Appli e 16, Appli e 16, Appli e 65, Appli e 65, Appli e 65, Appli e 17, Appli e 11, Appli e 12, Appli
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WRSSI WRSSI WRSSI LSPOI LSPOI LSPOI KVKFI KVKFI HHH KVKFI	8-12 2, Applica 6852849 FORMATION: RESCRITS: TISIEN, Campbel INVENTION: RENCE: REG PPLICATION ILING DATE SEQ ID NO PATENTIALION PATENTIALION PATENTIALION ILING DATE SEQ ID NO PATENTIALION PATENTIALION ILING DATE SEQ ID NO PATENTIALION PATENTIALION ILING DATE SEQ ID NO PATENTIALION ILING DATE ILING DATE I		11111111111111111111111111111111111111
Conserva           sknviker  sknviker  ofoygskv          ofoygskv  celgvneps           skkevoleg	38-12 12, Application 12, Application 12, Application 13, Application 15, Application 17, REGENTS OF 17, TSIEN, Ro, 17, Campbell, 11, INVENTION IN ERENCE: REGEN: APPLICATION IN FILING DATE: F SEQ ID NOS: F SEQ ID NOS: 12, 225 225 RT M: Discosoma M: Discosoma 38-12 Ch Similarity		M & 7 B W W O O O O O O O O O O
	18-12 12, Application US/0986653 16, Application US/0986653 16, Application US/0986653 16, Application US/0986653 17: REGENTS OF THE UNIVERSITE TRIEN, ROGET 11 TOTAL NON-OLIGOMERIZ 12 ERENCE: REGEN1530-2 12 FILING DATE: 2001-05-24 17 ESQ ID NOS: 29 18 PET DISCOSOMA SP. 12 1018COSOMA SP. 138-12 1018COSOMA SP.		000000000000000000000000000000000000000
tive 0; Mismatci	rion US/09866538  F THE UNIVERSITY ( Robert NON-OLIGOMERIZING SUS/09/866 2001-05-24 S: 29. Version 3.0  100.0%; Score y 100.0%; Pred.		2338 2238 2238 2238 2238 2239 2231 2232 2338 2338 2338 2338
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hes 0; Indels 0; Gaps  GEGGGRPYEGHNTVKLKVTKGGPLPFAWD	•		20 32 132 132 132 133 145 155 157 157 157 157 157 157 157 157 15
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60 60 120 120 180			

RESULT 2
US-09-865-291-12
; Sequence 12, Application US/09865291
; Patent No. 6900304
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TING, Alice
; APPLICANT: ZHANG, Jin

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RESULT 3
US-10-152-296-2
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Patent No. 6723537
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CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 225
TYPE: PRT
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Best Local S
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PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Peelle, Beau
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells
FILE REFERENCE: 021044-000110US
CURRENT APPLICATION NUMBER: US/10/152,296
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                        FEATURE: FEATURE: Or Artificial Sequence:mammalian OTHER INFORMATION: Codon-optimized variant (DerED) of Discosoma OTHER INFORMATION: "red" red fluorescent protein (RFP)
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TYPE: PRT
ORGANISM: Artificial Sequence
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hes 224;
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Local Similarity 100.0%;
hes 225; Conservative 0
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                                                                                                                                                                                                                                                              Similarity
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                            KVKFIGVNEPSDGFVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 121
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          KVKF1GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE1HKALKLKDGGHYLVEFKS1
                                                                                                                                                                                                                                                            99.7%;
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Pred. No. 9.5e-132;
1; Mismatches 0;
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Pred. No. 3e-132;
; Mismatches 0;
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APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACII
CURRENT APPLICATION NUMBER: US/09/277,716A
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER FILING DATE: 1998-06-15
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 238
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US-09-277-716-16
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US-10-244-779-2
                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09277716A Patent No. 6232107 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Applicat Patent No. 6933375 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 123;
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Best Local
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TITLE OF INVENTION: Dolypeptides, Antibodies and Methods of Use Thereof
FILE REFERENCE: Rut 00-0123US
CURRENT APPLICATION NUMBER: US/10/244,779
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/322,189
PRIOR APPLICATION NUMBER: 609-14
NUMBER OF SEQ ID NOS: 16
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APPLICANT: Chen, Yi-Bu
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ilarity 57.2%;
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Pred. No. 1.7e-70;
6; Mismatches 56;
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APPLICANT: EXPAIL STUCE
APPLICANT: SZENT-GYOTGY1, Christopher
APPLICANT: SZENT-GYOTGY1, Christopher
APPLICANT: SZENT-GYOTGY1, Christopher
ITILE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
TITLE OF INVENTION: SCREENING AND THE USE THEREOF IN DIAGNOSTICS, HIG
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIG
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
CURRENT FILING DATE: 1990-03-26
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER: DATE: 1998-03-27
NUMBER: PRIOR PRICATION NUMBER: 60/079,624
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NUMBER: PRIOR PRICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER: PRIOR FILING DATE: PRIOR
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US-09-609-161B-16
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ORGANISM: Remilla mulleri
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Renilla mulleri FEATURE:
                                                                                                                                                                                                                                                                                                                                                                     / Match 40.0%; Score 485.5; DB 2;
Local Similarity 44.5%; Pred. No. 8.5e-48;
43; Mismatches 71;
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119 IYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFK 178
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o. 6436682
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97; Conserv
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                                                                                                       DIVSPAFQYGNRTFTKYPNDISDYFIQSFPAGFMYERTLRYEDGGLVEIRSDINLIEDKF 121
                                                                                                                                                DILSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCF 118
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44.5%; Pred. No. 8.5e-48;
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RESULT 7
US-09-626-581D-65
; Sequence 65, Application US/09626581D
parant No. 6548249
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                                    ; LENGTH: 238
; TYPE: PRT
; ORGANISM: Renilla muelleri
US-09-415-765B-65
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                                                                                                           GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Fusions of Scaffold Proteins with Random
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
CURRENT APPLICATION NUMBER: US/09/415,765B
CURRENT APPLICATION NUMBER: US/09/415,765B
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
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Query Match
                                                                                                                                                                                                                                                                                                                                                   Patent No. 6548632
                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Application US/09415765B
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Local Similarity 44.5%;
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    40.0%;
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; Pred. No. 8.5e-48;
43; Mismatches 71
    Score 485.5;
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US-09-626-580C-65
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                                                                                                                                                      RESULT 10
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Best Local S
Matches 97
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APPLICANT: Anderson, David
APPLICANT: Anderson, David
APPLICANT: Begenberger, Jakob M.
APPLICANT: Begenberger, Jakob M.
APPLICANT: Beele, Beau R.

TITLE OF INVENTION: FUSIONS OF SCAFFOLD PROTEINS WITH RANDOM PEPTIDE LIBRARIES
FILE REFERENCE: A-66900-2/RMS/AMS
CURRENT APPLICATION NUMBER: US/09/626,580C
CURRENT APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
                                                                 Sequence 3, Application US/09977897 Patent No. 6780974 GENERAL INFORMATION:
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APPLICANT: Chen, Yih-Tai
APPLICANT: Cao, Longguang
TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluoresce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 238
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                                                                                                                                                                                                                                                             SIYMAKKPV-QLPGYYYVDSKLDITSHNEDYTIVEQYE 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKQILKNTCLQEVMSYKVNLEGIVNNHVFTMEGCGKGNILFGNQLVQIRVTKGAPLPFAF 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.0%; Score 485.5; DB 2
44.5%; Pred. No. 8.5e-48;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 224
TYPE: PRT
ORGANISM: Ptilosarcus gurneyi
US-09-977-897-3
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; TYPE: PRT
; ORGANISM: Ptilosarcus
US-09-977-897-13
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APPLICANT: Chen, Yih-Tai
APPLICANT: Chen, Yih-Tai
APPLICANT: Chen, Yih-Tai
APPLICANT: Chen, Yih-Tai
APPLICANT: Chen, Longquang
TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescer
TITLE OF INVENTION: Protein with codon preference of mammalian expression systems and
FILE REFERENCE: 41856-5
CURRENT APPLICATION NUMBER: US/09/977,897
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 224
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                                                                                                                                                                                                                                                                                                                                    y Match 39.0%; Score 473.5; DB 2;
Local Similarity 45.5%; Pred. No. 1.9e-46;
hes 97; Conservative 40; Mismatches 73;
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                                                                                  YRGNGFPSNGPVMQKAILGMEPSFEVVYMNSGVLVGEVDLVYKLESGNYYSCHMKTFYRS
                                                                                                                                                                                                          QFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVK 123
                                                                                                                                                                                                                                                    KNTGLKEIMSAKASVEGIVNNHVFSMEGFGKGNVLFGNQLMQIRVTKGGPLFFAFDIVSI 67
                                                                                                                                                                                                                                                                                             KNV-IKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSP 63
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  KGGVKEFPEYHFIHHRLEKT-YVEEGSFVEQHE
                                       KKPV-QLPGYYYVDSKLDITSHNEDYTIVEQYE 215
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45.5%; Pred. No. 1.9e-46;
40. Mismatches 73;
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; TYPE: PRT; ORGANISM: Ptilosarcus
US-09-977-897-14
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US-09-977-897-14
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US-09-977-897-15
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Best Local S
Matches 97
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APPLICANT: Chen, Yih-Tai
APPLICATION: A synthetic DNA encoding an orange seapen-derived green fluoresce
TITLE OF INVENTION: protein with codon preference of mammalian expression systems and
FILE REFERENCE: 41856-5
CURRENT APPLICATION NUMBER: US/09/977,897
CURRENT APPLICATION NUMBER: US/09/977,897
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 226
TYPE: PRT
ORGANISM: Ptilosarcus gurneyi
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APPLICANT: Cao, Longguang
TITLE CAO, Longguang
TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluoresce
TITLE OF INVENTION: protein with codon preference of mammalian expression systems an
FILE REFERENCE: 41856-5
CURRENT APPLICATION NUMBER: US/09/977,897
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
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68 AFQYGNRTFTKYPDDIADYFVQSFPAGFFYERNLRFEDGAIVDIRSDISLEDDKFHYKVE 127
                                     64 QFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNPEDGGVVTVTQDSSLQDGCFIYKVK 123
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                                                                                           KNTGLKEIMSAKASVEGIVNNHVFSMEGFGKGNVLFGNQLMQIRVTKGGPLPFAFDIVSI 67
                                                                                                                                     KNV-IKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSP
                                                                                                                                                                                       39.0%; Score 473.5; DB 2;
45.5%; Pred. No. 1.9e-46;
ative 40; Mismatches 73;
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US-09-977-897-16
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US-09-977-897-16
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US-09-977-897-17
                                                                                                                  ; ORGANISM: Ptilosarcus gurneyi
US-09-977-897-17
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GENERAL INFORMATION:
APPLICANT: Chen, Yih-Tai
APPLICANT: Chen, Yih-Tai
APPLICANT: Chen, Longguang
TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescer
TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescer
TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescer
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CURRENT APPLICATION NUMBER: US/09/977,897
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
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Best Local Similarity 45.5%; Pred. No. 1.9e-46;
Matches 97; Conservative 40; Mismatches 73
Best Local Similarity
                                          Query Match
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APPLICANT: Cao, Longguang
TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescer
TITLE OF INVENTION: protein with codon preference of mammalian expression systems and
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Score 473.5; DB Pred. No. 2e-46;
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11B_PUBCOMB.pep:*

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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-845-484-3
US-10-855-988-12
US-10-865-988-12
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					SULT 1  O9-99-745-67  O9-99-745-67  Bequence 67, Application US/ Batent No. US20020157120A1  BAPPLICANT: THE REGENTS OF TAPPLICANT: THE REGENTS OF TOPPLICANT: Baird, Geoffrey TITLE OF INVENTION: CIRCULA  FILE REFERENCE: REGEN1470-1  CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-  PRIOR APPLICATION NUMBER: 0  PRIOR FILING DATE: 199-05-  RIOR FILING DATE: 199-05-  RIOR FILING DATE: 199-05-  RIOR FILING DATE: 199-05-  PRIOR FILING DATE: 199-		
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US-09-66-538-12
Sequence 12, Application US/09866538
Publication No. US20030032088A1
GENERAL INFORMATION:
APPLICANT: RECENTS OF THE UNIVERSITY OF CALIFORNIA;
APPLICANT: TSIEN, Roger

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CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 225
TYPE: PRT
ORGANISM: Discosoma sp.
US-09-866-538-12
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; TYPE: PRT
; ORGANISM: Discosoma sp.
US-09-794-308-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILLING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGEN1530-2
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                                                            KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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ZACHARIAS, Davi
BAIRD, Geoffrey
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APPLICANT: Lukyanov, Sergey A
APPLICANT: Fradkov, Arcady F.
APPLICANT: Fradkov, Arcady F.
APPLICANT: Habas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terskith, Alexey
FITLE DF INVENTION: Mcthods for Using the Same
FILE OF INVENTION: Mcthods for Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
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CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 225
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Publication No. US20030186229A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 225; Conserv
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Publication No. US20020197676A1
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APPLICANT: TING, Alice
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
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ORGANISM: Discosoma
APPLICATION NUMBER: 09/444,338 FILING DATE: 1999-11-19
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181 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225

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; LENGTH; 225
; TYPE; PRT
; ORGANISM; Discosoma species
US-10-006-922-12
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; ORGANISM: Discosoma
US-10-081-864-8
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GENERAL INFORMATION:

APPLICANT: Lukyanov, Konstantin

APPLICANT: Lukyanov, Konstantin

APPLICANT: Yanushevich, Yuriy

APPLICANT: Savistky, Alexandr

APPLICANT: Pradkov, Arcady

TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins

TITLE OF INVENTION: Methods for Using the Same

TILE REPERENCE: CLON-067

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: 10/006,922

PRIOR APPLICATION NUMBER: 10/006,922

PRIOR TILING DATE: 2001-12-04

PRIOR TILING DATE: 2001-12-04
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Best Local Similarity 100.0%;
Matches 225; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/270,983
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 225
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Publication No. US20030022287A1
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YMAKKPYQLPGYYYYDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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                                                                                  KVKFIGVNFPSDGFVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                           KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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                                                                                                                                                                                                                                                                                      100.0%; Score 1214; DB 4; 100.0%; Pred. No. 6.6e-114; tive 0; Mismatches 0;
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Pred. No. 6.6e-114;
Mismatches 0;
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Sequence 2, Application US/10315920

| Publication No. US20030175809A1
| GENERAL INFORMATION:
| APPLICANT: Teradkov, Arcady Fedorovich
| APPLICANT: Terskikh, Alexey
| TITLE OF INVENTION: FLUCRESCENT TIMER PROTEINS AND METHODS
| TITLE OF INVENTION: FOR THEIR USE
| FILE REFERENCE: CLON-077CIP
| CURRENT APPLICATION NUMBER: US/10/315,920
| CURRENT FILING DATE: 2002-12-09
| PRIOR APPLICATION NUMBER: 60/211,607
| PRIOR APPLICATION NUMBER: FOT/US01/19097
| PRIOR APPLICATION NUMBER: FOT/US01/19097
| PRIOR APPLICATION NUMBER: SOT/US01/19097
| PRIOR FILING DATE: 2001-06-13
| NUMBER: OF SEQ ID NOS: 22
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
| LENGTH: 225
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US-10-315-920-2
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SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 1
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Publication No. US2003005005777
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Best Local Similarity
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APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONDERIC AND DIMERIC
TITLE OF INVENTION: PROTEIN VARIANTS AND
FILE REFERENCE: UC083.1CP2CPL
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
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PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(225)
OTHER INFORMATION: wild-type DsRed
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ORGANISM: Discosoma
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METHODS FOR
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RESULT 10
US-10-370-570-56
; Sequence 56, Application US/10370570
; Publication No. US20030219717A1
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US-10-132-067-4
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US-10-315-920-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: red fluorescent protein (dsRED)
US-10-132-067-4
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Publication No. US20030203355A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 225; Conserv
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APPLICANT: Zeytun, Ahmet
APPLICANT: Zeytun, Ahmet
APPLICANT: Waldo, Geoffrey
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fluorobodies: Binding Ligands With Intrinsic
TITLE OF INVENTION: Fluorescence
FILE REFERENCE: 021362-000600US
CURRENT APPLICATION NUMBER: US/10/132,067
CURRENT APPLICATION NUMBER: US/10/132,067
CURRENT FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 225
TYPE: PRT
ORGANISM: Discosoma sp.
FEATURE:
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                                                                                                                                                     YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                  KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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APPLICANT: DAHL, Soren Weis et al.

TITLE OF INVENTION: FLUOROPHORE COMPLEMENTATION PROFILE REFERENCE: 3759-0130P

CURRENT APPLICATION NUMBER: US/10/370,570

CURRENT FILING DATE: 2003-02-24

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2

SEQ ID NO 56

LENGTH: 225

TYPE: PRT
ORGANISM: Discosoma sp.

US-10-370-570-56
                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 016285-34-1
CURRENT APPLICATION NUMBER: US/10/406,618
CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: US 60/387,968
PRIOR FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/370,598
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 225
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                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Spontaneously; OTHER INFORMATION: fluororescent protein DsRed.
US-10-406-618-32
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                                                                                                                                                                      Query Match
Best Local S
Matches 225
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Best Local :
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APPLICANT: Ip, Denis Tsz-Ming
APPLICANT: The Chinese University of Hong Kong
TITLE OF INVENTION: No. US20030219814A1el Fluorescent Proteins
                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                      / Match 100.0%; Score 1214; DB 4; Local Similarity 100.0%; Pred. No. 6.6e-114; nes 225; Conservative 0; Mismatches 0;
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LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                      LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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Pred. No. 6.6e-114;
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Sequence 7, Application US/10311030

Publication No. US20040171107A1

GENERAL INFORMATION:
APPLICANT: Nelson, David
APPLICANT: Tsien, Roger
ITITLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS
FILE REFERENCE: 15916-032US1
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US/10/311,030
CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/184,732
PRIOR PILING DATE: 2001-02-23
INUMBER OF SEQ ID NOS: 12
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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Publication No. US20040115792A1

GENERAL INFORMATION:
APPLICANT: Lichtenberg-Frate, Hella
TITLE OF INVENTION: YEAST STRAIN FOR TESTING THE GENOTOXICITY AND CYTOTOXICITY OF
TITLE OF INVENTION: COMPLEX ENVIRONMENTAL CONTAMINATIONS
FILE REFERENCE: 1487/3

CURRENT APPLICATION NUMBER: US/10/433,640

CURRENT APPLICATION NUMBER: PCT/EP01/14610
PRIOR APPLICATION NUMBER: PCT/EP01/14610
PRIOR APPLICATION NUMBER: DE 10061872.3
PRIOR APPLICATION NUMBER: DE 10061872.3
PRIOR APPLICATION NUMBER: DE 2001-12-12

PRIOR APPLICATION NUMBER: DE 10061872.3
PRIOR PILING DATE: 2001-12-12

PRIOR PILING DATE: 2001-12-12
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US-10-433-640-13
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TYPE: PRT
ORGANISM: Discosoma sp
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APPLICANT: Bulina, Maria
APPLICANT: Chudakov, Dmitry
APPLICANT: Chudakov, Dmitry
APPLICANT: Lukyanov, Konstantin
TITLE OF INVENTION: Methods for Making and Using the Same
FILE REFERENCE: CLOW 092
CURRENT APPLICATION NUMBER: US/10/845,484
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/343128
PRIOR APPLICATION NUMBER: 60/343128
PRIOR APPLICATION NUMBER: PTUSO2/41418
PRIOR FILING DATE: 2002-12-23
SOPTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma 6
US-10-845-484-3
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US-10-845-484-3
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Best Local Similarity 100.0%;
Matches 225; Conservative 0
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Publication No. US20040248180A1
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Best Local (
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Pred. No. 6.6e-114;
0; Mismatches 0;
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Sequence 12, Application US/10885988

Publication No. US20040259165A1

GENERAL INFORMATION:

APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: TSIEN, ROGET

APPLICANT: Campbell, Robert

TITLE OF INVENTION: NON-OLIGOMERIZING FLUCRESCENT PROTEINS

FILE REFERENCE: REGEN1530-2

CURRENT APPLICATION NUMBER: US/10/885,988

CURRENT FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: US/09/866,538

PRIOR APPLICATION NUMBER: US/09/866,538

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.0

SEQ ID NO 12

LENGTH: 225

TYPE: PRT

ORGANISM: Discosoma sp.
Search completed: January 11, 2006, 02:06:37 Job time: 63 secs
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US-10-885-988-12
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/USOS_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USOS_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
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   Match
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-209-208-6
US-10-209-208-79
US-10-209-208-79
US-11-179-411-32
US-11-179-411-32
US-11-179-411-33
US-11-179-208-11
US-11-209-208-15
US-11-032-236-6
US-11-032-236-6
US-11-032-236-13
US-10-209-208-13
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PRIOR APPLICATION NUMBER: 09/866,538
PRIOR PILLING DATE: 2001-05-24
PRIOR PELLING DATE: 2001-05-24
PRIOR PELLING DATE: 2001-02-26
PRIOR FILLING DATE: 2001-02-26
NUMBER: PSEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 225
TYPE: PRT
ORGANISM: Discosoma sp.
FEATURE:
NAME/KEY: misc feature
COCATION: (1)...(225)
OTHER INFORMATION: wild-type DsRed
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181 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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                                                   KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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Sequence 4, Application US/10209208

Publication No. US20050244921A1

GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
ITILE OF INVENTION: FOR MAKING SAME
FILE OF INVENTION: FOR MAKING SAME
CURRENT APPLICATION NUMBER: US/10/209,208

CURRENT APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/794,308

PRIOR APPLICATION NUMBER: 09/794,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/10209208 Publication No. US20050244921A1
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PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS TITLE OF INVENTION: FOR MAKING SAME FILE REFERENCE: UCO83.1CP2CP2 CURRENT APPLICATION NUMBER: US/10/209,208 CURRENT FILING DATE: 2002-07-29 PRIOR ARPLICATION NUMBER: 10/121,258 PRIOR FILING DATE: 2002-04-10 PRIOR FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Campbell, Rober APPLICANT: Geoffrey Baird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Taien,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1207; DB 6;
Pred. No. 1.1e-109;
0; Mismatches 1;
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APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FOR MAKING SAME
FILE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.LCP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
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; OTHER INFORMATION: DsRed polypeptide variant
US-10-209-208-4
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US-10-209-208-24
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LENGTH: 225
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Best Local Similarity
Matches 216; Conserv
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Publication No. US20050244921A1
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                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Campb
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                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Dered polypeptide variant "T1" with I125R mutation
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
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les 215; Conserv
  121 KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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                                                                                                                                     1 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDI
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                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
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                                                                                                                                                                                         Score 1153; DB 6;
Pred. No. 1.8e-104;
3; Mismatches 7;
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Pred. No. 3.7e-105;
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                                                                                                                                                                                                                               Length 225;
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APPLICANT: Campbell Robert
APPLICANT: Campbell Robert
TITLE OF INVENTION: FULORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR PILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/966,538
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
Sequence 8, Application US/10209208

Publication No. US20050244921A1

GENERAL INFORMATION:
APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FOR MAKING SAME
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
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                                                                                                                                                                                                                                                                                           US-10-209-208-8
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Publication No. US20050244921A1
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; Pred. No. 2.2e:
7; Mismatches
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                                                                                                                                          AND
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61 LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120

1 MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI

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APPLICANT: Teien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS ANI
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UCO83.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
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US-10-209-208-79
                                                                                                                                       ; OTHER INFORMATION: DsRed polypeptide variant "mRFP1.1" US-10-209-208-79
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PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR PRIOR DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 79, Application US/10209208
Publication No. US20050244921A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                               Query Match
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 80
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                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                         LENGTH: 225
                                                                            Local Similarity
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                                                           190;
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1 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDI 60
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                                                                            Score 1012; DB 6; Length 225; Pred. No. 7.4e-91;
                                                             Mismatches
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RESULT 9
US-11-175-766-16
; Sequence 16, Application US/11175766
; Publication No. US20050272111A1
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; TYPE: PRT
; ORGANISM: Renilla mulleri
US-11-179-411-16

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US-11-179-411-16
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LENGTH: 238
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH 7
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-128
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CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US/09/808,898
PRIOR FILING DATE: 2001-03-15
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR APPLICATION NUMBER: 60/189,691
OR FILING DATE: 2000-03-15
OR APPLICATION NUMBER: 09/277,716
OR APPLICATION NUMBER: 09/277,716
OR FILING DATE: 1999-03-26
OR APPLICATION NUMBER: 08/757,046
OR APPLICATION NUMBER: 08/597,274
OR FILING DATE: 1996-01-08/597,274
OR APPLICATION NUMBER: 08/908,909
OR APPLICATION NUMBER: 08/908,909
OR APPLICATION NUMBER: 08/900,103
OR APPLICATION NUMBER: 08/990,103
OR APPLICATION NUMBER: 08/990,103
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                                                                                                                TLMKSKGVVKEFPSYHFIQHRLEKT-YVEDGGFVEQHE
                                                                                                                                                 SIYMAKKPV-QLPGYYYVDSKLDITSHNEDYTIVEQYE 215
                                                                                                                                                                                                                           IYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFK 178
                                                                                                                                                                                                                                                                  DIVSPAFQYGNRTFTKYPNDISDYFIQSFPAGFMYERTLRYEDGGLVEIRSDINLIEDKF
                                                                                                                                                                                                                                                                                                                                    SKQILKNTCLQEVMSYKVNLEGIVNNHVFTMEGCGKGNILFGNQLVQIRVTKGAPLFFAF 61
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/11/175,766
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: US/09/808,898
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/189,691
PRIOR FILING DATE: 2000-03-15
PRIOR PPLICATION NUMBER: 09/277,716
PRIOR PPLICATION NUMBER: 09/277,716
PRIOR PPLICATION NUMBER: 09/57,046
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 08/597,274
PRIOR PPLING DATE: 1996-11-25
PRIOR PPLICATION NUMBER: 08/597,274
PRIOR FILING DATE: 1996-02-06
PRIOR APPLICATION NUMBER: 08/990,103
PRIOR PRILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 08/990,103
PRIOR PILING DATE: 1997-12-12
PRIOR PPLICATION NUMBER: 08/990,103
PRIOR PRILING DATE: 1997-12-12
CURRENT APPLICATION NUMBER: US/11/179,411
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US/09/808,898
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/189,691
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-03-277,716
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR APPLICATION NUMBER: 09/277,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/11179411 Publication No. US20050266491A1 GENERAL INFORMATION:
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
                                                                                                                                                                                                                                                                  APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLBIC ACIDS ENCODING
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-128
FILE REFERENCE: 24729-128
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SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 08/757,046
PRIOR FILING DATE: 1996-11-25
PRIOR APPLICATION NUMBER: 08/597,274
PRIOR APPLICATION NUMBER: 08/597,274
PRIOR APPLICATION NUMBER: 08/908,909
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 08/990,103
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOUTWARE: PSSETSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 238
TYPE: PRT
ORGANISM: Ptilosarcus gurneyi
US-11-179-411-32
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; TYPE: PRT
; ORGANISM: Ptilosarcus
US-11-175-766-32
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                                                                               PRIOR APPLICATION NUMBER: 08/990,103
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FRETSEQ for Windows Version
SEQ ID NO 32
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CURRENT FILING DATE: 2005-07-06
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgiak, William
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: FLOURESCENT POTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH T
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-128
                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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APPLICATION NUMBER: 09/277,716
FILING DATE: 1999-03-26
APPLICATION NUMBER: 08/757,046
FILING DATE: 1996-11-25
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                                                                                                                                                                                                                 APPLICATION NUMBER: 08/908,909
                                                                                                                                                                                               FILING DATE: 1997-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFQYGNRTFTKYPDDIADYFVQSFPAGFFYERNLRFEDGAIVDIRSDISLEDDKFHYKVE
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RESULT 12
US-11-179-411-27
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Best Local
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szczepaniak, William
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PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR FILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1996-11-25
PRIOR PILING DATE: 1996-11-25
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CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US/09/8008,898
PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING TITLE OF INVENTION: FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/597,274
PRIOR FILING DATE: 1996-02-06
PRIOR APPLICATION NUMBER: 08/908,909
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 08/990,103
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2:
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                 Local
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                                           121 KVKFIGVNFPSDGPVNOKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 AFQYGNRTFTKYPDDIADYFVQSFPAGFFYBRNLRFEDGAIVDIRSDISLEDDKFHYKVE
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                                                                                                                 61 LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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97; Conservative
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NVDFKAKDLRRMGPVMQQDIVGMQPSYESMYTNVTSVIGECIIAFKLQTGKHFTYHMRTV
                                                                                     VSVAFSYGNRAYTGYPEEISDYFLQSFPEGFTYERNIRYQDGGTAIVKSDISLEDGKFIV
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                                                                                                                                                                          MDLAKLGLKEVMPTKINLEGLVGDHAFSMEGVGEGNILEGTQEVKISVTKGAPLPFAFDI
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45.5%;
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40.5%; Pred. No. 6.9e-34;
7ative 38; Mismatches 93
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Pred. No. 8.3e-39;
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RESULT 13
US-11-175-766-27
; Sequence 27, Appl
; Publication No. I
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US-11-179-411-33
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Sequence 33, Application US/11179411

Publication No. US20050266491A1

GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szezepaniak, William
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH T
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 27
LENGTH: 233
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CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: US/09/808,898
PRIOR FILING DATE: 2001-03-15
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-03-15
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APPLICANT: Szent-Gyorg
APPLICANT: Szczepaniak
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TITLE OF INVENTION: FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS,
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
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TYPE: PRT
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FILING DAYE: 1999-03-26
APPLICATION NUMBER: 08/757,046
FILING DAYE: 1996-11-25
APPLICATION NUMBER: 08/597,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/990,103
FILING DATE: 1997-12-12
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Szczepaniak, William
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; TYPE: PRT
; ORGANISM: Renilla
US-11-179-411-33
PRIOR APPLICATION NUMBER: US/09/808,898
PRIOR PILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/189,691
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1996-11-25
PRIOR APPLICATION NUMBER: 08/757,274
PRIOR PILING DATE: 1996-02-06
PRIOR PILING DATE: 1996-02-06
PRIOR APPLICATION NUMBER: 08/908,909
PRIOR APPLICATION NUMBER: 08/908,909
PRIOR APPLICATION NUMBER: 08/908,909
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CURRENT FILLING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US/09/808,898
PRIOR PELING DATE: 2001-03-15
PRIOR PILLING DATE: 2001-03-15
PRIOR PILLING DATE: 2001-03-15
PRIOR PILLING DATE: 2001-03-15
PRIOR PILLING DATE: 1990-03-16
PRIOR PILLING DATE: 1990-03-26
PRIOR PILLING DATE: 1999-03-26
PRIOR PILLING DATE: 1996-11-25
PRIOR PILLING DATE: 1996-11-25
PRIOR PILLING DATE: 1996-10-20-06
PRIOR PILLING DATE: 1996-01-25
PRIOR PILLING DATE: 1996-02-06
PRIOR PILLING DATE: 1996-02-06
PRIOR PILLING DATE: 1997-08-08
PRIOR PILLING DATE: 1997-08-08
PRIOR PILLING DATE: 1997-08-08
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH T
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-128
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/175,766
CURRENT FILING DATE: 2005-07-06
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SOFTWARE: Fast
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FastSEQ for Windows Version
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40.1%; Pred. No. 9.9e-33;
27. Mismatches 95;
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APPLICATION NUMBER: 08/908,909
FILING DATE: 1997-08-08
APPLICATION NUMBER: 08/990,103

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| PRIOR FILING DATE: 1997-12-12 | NUMBER OF SEQ ID NOS: 33 | SOFTWARE: FREEED for Windows Version 4.0 | SEQ ID NOS: 33 | ENGIFY 233 | ENGIFY: 233 | ENGIFY: 233 | TYPE: PRT | ORGANISM: Renilla Reniformis mutein | US-11-175-766-33 | 33.8%; Score 410.5; DB 7; Length 233; DR-11-175-766-33 | Gaps 1; ORGANISM: Renilla Reniformis mutein | US-11-175-766-33 | Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 89; Conservative 37; Mismatches 95; Indels 1; Gaps 1; Matches 95; Indels 1; Gaps 1;
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-MODEL-frame+ p2n.model -DEV=xlp
-Q-/cgn2 1/USPTO_spool_p/US10006922/runat_10012006_162408_18921/app_query.fasta_1.391
-Q-/cgn2 1/USPTO_spool_p/US10006922/runat_10012006_162408_18921/app_query.fasta_1.391
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-DEV_TIMEOUT=10 -YGAPOP=10 -YGAPOP=10 -YGAPOP=6
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## ALIGNMENTS

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	AR183915.1	GI:20227884					
WORDS	•						
RCB	Unknown.						
RGANISM	Unknown.						
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ERENCE	1 (bases 1 to 678)	L to 678)					
	Taien, R.Y.	Tsien, R.Y. and Gonzalez, J.E. III.	LE. III.				
	Detection o	Detection of transmembrane potentials by optical methods	le potential	вьу	optical	method	60
2	Patent: US	Patent: US 6342379-A 6 29-JAN-2002;	-JAN-2002;				
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ry Match:	1	100.00%	Indels:		0		
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                                                                                                                         Discosoma sp.
Discosoma sp.
Bukaryota; Metazoa; Cnidaria; Anth
Bukaryota; Metazoa; Discosomatidae;
                                                 Tsien,R.Y. and Gonzalez,J.E.

Detection of transmembrane potentials by opt
Patent: WO 0142211-A 6 14-JUN-2001;
The Regents of the University of California
Location/Qualifiers
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Stack, J.H., Whitney, M., Cubitt, A.B. Methods of protein destabilization a
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Biosciences Corporation (US)
Location/Qualifiers
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Fluorescent timer proteins and methods
Patent: WO 0196373-A 1 20-DEC-2001;
Clontech Laboratories Inc. (US)
Location/Qualifiers
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Sequence 1 from Patent WO0196373.
AX370404 GI:18857490
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Corallimorpharia; Discosomatidae; Discosoma.
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/mol_type="unassigned '
/db_xref="taxon:86600"
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Matz,M.V., Fradkov,A.F., Labas,Y.A., Savitsky,A., Markelov,M.L. and Lukyanov,S.A.
Direct Submission
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Discosoma sp.
Eukaryota, Metazoa, Chidaria, Anthozoa, Zoantharia,
Corallimorpharia, Discosomatidae, Discosoma.
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Matz, M.V., Fradkov, A.F., Labas, Y.A., Savitsky, A.P.,
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Discosoma sp. fluorescent
AF168419
AF168419.2 GI:7105733
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Sequence update by submitter
On Feb 25, 2000 this sequence version
Location/Qualifiers
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/protein_id="AAF03369.1"
/db_xref="GI:6090867"
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Tsien,R.Y. and Campbell,R.E.
Non-oligomerizing tandem fluorescent proteins
Patent: US 6852849-A 11 08-FEB-2005;
The Regents of the University of California; (
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Telen,R.Y., Ting,A.Y. and Zhang,J.
Emission ratiometric indicators of phosphorylation
Patent: US 6900304-A 11 31-MAY-2005;
The Regents of the University of California; Oakland,
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Corallimorpharia; Discosomatidae; Discosoma.
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                                                                                                                                                                          LygValLygPheIleGlyValAgnPheProSerAgpGlyProValMetGlnLygLygThr
                                                                                                                                                                                                               AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
                                                                                                                                                                                                                                                                                                                                               LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                  CACAACACCGTGAAGCTTAAGGTGACCAAGGGCGGCCCCTGCCCTTCGCCTGGGACATC
                                                                                                                                    HisAsnThrVallysLeuLysValThrLysGlyClyProLeuProPheAlaTrpAsplle 60
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                                                                                                                                                                                            ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
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                                                                                                                                                                                                                                                       MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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Modified fluorescent proteins
Patent: WO 0162919-A 51 30-AUG-2001;
Aurora Biosciences Corporation (US)
Location/Qualifiers
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other sequences; artificial sequences.
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Centre National De La Recherche Scientifique-CNRS (FR); UNIVERSITE CLAUDE BERNARD - LYON 1 (FR); Institut National de la Recherche Agronomique (INRA) (FR)
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Chavancy,G., Couble,P., Durand,B., Grenier,A.M., Horard,B., Julien,B., Mauchamp,B., Nony,P., Prudhomme,J.C. and Royer,C. Nucleic acid controlling the expression of a useful polypeptide the posterior silk glands of a lepidoptera and application there Patent: WO 2004083445-A 3 30-SEP-2004;
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                                                                                                                                                                                IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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                                                                              IleThrSerHisAsnGlwAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
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-Q=/cgn2_1/USPTO_spool_p/USI0006922/runat_10012006_162408_18913/app_query.fasta_1.391
-Da-N Genceeq -QEMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTENT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US10006922_@CGN 1 1 1096 @runat_10012006_162408_18913 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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## RESULT 1 AAH47654 ID AAH4 AAH47654 standard; cDNA; 678 BP WPI; 2001-557704/62 Nelson D, 13-FEB-2001; 2001WO-US004625. 30-AUG-2001. WO200162919-A1 Discosoma sp. Fluorescent protein; Anthozoan; Discosoma sp. red drFP583 protein coding sequence. 30-NOV-2001 AAH47654; 23-FEB-2000; 2000US-0184732P. (AURO-) AURORA BIOSCIENCES CORP Zamaira E, (first entry) fluorescence; marker; FRET; drfP583; ss

ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-10-006-922A-12 (1-225) Score invention can be expressed by standard recombinant methodology. (II) are used a fluorescent markers and FRET partners. It is used for identifying protein-protein interactions. (II) is also suitable for multiplexed fluorescent analysis and FRET-based applications using existing Aequorea fluorescent proteins. (II) has improved brightness, reduced spectral cross talk, and is rapidly and efficiently expressed in mammalian cells. The key mutations in the encoding nucleic acids provide improved folding, brightness, and create (II) with sharper, more defined excitation and emission peaks when expressed in mammalian cells. The present sequence represents the coding sequence of a Discosoma sp. drFP583 protein, an Sequence 678 The invention provides a nucleic acid encoding functional red fluores CC protein (II) that differs from the sequence of an Anthozoan red fluorescent protein by at least one amino acid substitution, and with different fluorescent properties. The red fluorescent protein of the anthozoan fluorescent protein Proteins for Fluorescence Resonance Energy Transfer (FRET) comprise functional red fluorescent proteins, and the encoding nucleic acids, key mutations for improving the proteins function. 8 0 :: 361 301 481 421 141 101 181 181 161 121 81 61 41 61 MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGACCTTTGCCATTTGCGTTGGGATATT ACGGTCAATGGGCACGAGTTTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGC ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly ATGAGGTCTTCCAAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGCATGGAAGGA IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrTyrValAspSerLysLeuAsp BP; 205 A; 129 2.3e-140 1214.00 100.00% 100.00% 100.00% x AAH47654 (1-678) 90pp; English. ç; 178 Length:
Matches:
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Mismatches:
Indels:
Gaps: <u>و</u> 166 H 0 σ; 678 0 225 0 0 0 Other; red fluorescent with 180 160 140 120 100 540 480 420 240 80 180 60 120 40 60

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                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                   The present invention relates to a method for destabilising a target protein in a cell. The method comprises a linker moiety which operatively couples a target protein (a reporter moiety) to a linear multimerised celestabilising domain, which is non-cleavable by a -NH-ubiquitin protein celedoproteases. The method is useful for detecting an activity such as compressed, protein kinase or phosphoprotein phosphatase activity and is celestage useful for identifying modulators of these activities. The method is celestage useful for developing novel assays for a wide range of post-celestage useful for developing novel assays for a wide range of post-celestage useful for developing novel assays for a wide range of post-celestage useful for developing novel assays proteolysis, phosphorylation, celestage celestage useful for developing novel assays for a wide range of post-celestage useful for developing novel assays for a wide range of post-celestage useful for developing novel assays for a wide range of post-celestage useful as disease proteolysis, phosphorylation, prenylation, celestage useful for creating celestage useful for creating celestage useful for creating celestage useful as disease models and transgenic plants with celestage useful as disease models and transgenic plants with celestage useful as disease models and transgenic plants with celestage useful as a natural fluorescent protein, dsFP483 celestage useful for creating celestage useful as a reporter moiety in the exemplification of the invention
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                                                                                                                                                                                                                                              Sequence 678
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capable of undergoing energy transfer by either donating or accepting excited state energy to the fluorescent ion. The membrane is then exposed to excitation light and the energy transfer between the reagents is measured and related to the membrane potential. The method is useful for detecting changes in membrane potential in subcellular organelle membranes in biological systems. The method is used for screening of test chemicals for activity to modulate the activity to of target ion channel. The invention also provides a transgenic organism comprising a first reagent that comprises a charged hydrophobic fluorescent molecule and a second reagent comprising a bioluminescent or naturally fluorescent protein. The present sequence is Discosoma species (red) DNA encoding an Anthozoa fluorescent protein (FP), drFP583
                                                                                                                                                                                                                                                                                                                                               The patent discloses optical methods and compositions for determining transmembrane potential across biological membranes in living cells. The method of determining the electrical potential across a membrane in a biological system comprises introduction of two reagents, a first reagen comprising a hydrophobic fluorescent ion capable of redistributing from first face of the membrane to a second face of the membrane in response to membrane potential change and a second reagent that label the first face or the second face of the membrane in complore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining electrical potential across a membrane in biological systems, comprises introducing two reagents, exposing the membrane to light and measuring the energy transfer.
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Alignment | Pred. No.: Percent Similarity:
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Query Match: Score: US-10-006-922A-12 (1-225) x AAD11142 (1-678) 2.3e-140 1214.00 100.00% 100.00% 100.00% Length: Matches: Conservative: Gaps: Indels: Mismatches: 678 0 0 0

Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

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The invention relates to DNA (I) containing either sequence ABA95905 o sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (YRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum o Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Escherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern biotechnology. (I) are optimised for expression in yeast and so genera RFP at higher levels with stronger fluorescence and thus lowers the detection limit and gives a better signal-to-noise ratio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence ABAS596 encoding a yeast optimised Red Fluorescent Protein (yRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum or Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Escherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern biotechnology. (I) are optimised for expression in yeast and so generate RFP at higher levels with stronger fluorescence and thus lowers the detection limit and gives a better signal-to-noise ratio. The present sequence is that of a polynucleotide encoding the yeast optimised RFP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA encoding red fluorescent protein, useful as marker biotechnology, has sequence optimized for expression in euk especially yeast or plants.
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The invention relates to DNA (I) containing either sequence ABA95905 sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (yRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum
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                          ABA95920
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 678 BP; 198 A; 147 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding red fluorescent protein, useful as marker biotechnology, has sequence optimized for expression in eulespecially yeast or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast; red fluorescent protein; RFP; plant; transgenic; GFP; Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis tha Escherichia coli; green fluorescent protein; biotechnology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 19pp; German.
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                                                                                                               HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                                                                                                                                                      ACUGUUAACGGUCACGAAUUCGAAAUCGAAGGUGAAGGUGAAGGUAGACCAUACGAAGGU
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AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                              UUGUCUCCACAAUUCCAAUACGGUUCUAAGGUCUACGUCAAGCACCCAGCUGACAUUCCA
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New nucleic acid encoding a non-aggregating chromo- or fluorescent of an aggregating Chidarian chromo- or fluorescent protein or mutan analyte detection assays or fluorescence activated cell sorting
                                 WPI; 2002-691654/74.
P-PSDB; AAE28833.
                                                                                            21-FEB-2001; 2001US-0270983P.
04-DEC-2001; 2001US-00006922.
                                                                                                                                                                                                                    D1scosoma
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Disclosure; Page 70; 80pp; English.

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CC The invention relates to nucleic acid molecules encoding non-aggregating CC chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are CC cuseful in analyte detection assays, as colouring agents, as markers in CC recombinant DNA applications, as sunscreens or filters, in fluorescence CC resonance energy transfer (FRET) applications, as biosensors in CC prokaryotic and eukaryotic cells, in screening assays, as second CC messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present CC in protein of the invention

XX

Sequence 678 BP; 146 A; 223 C; 203 G; 106 T; 0 U; 0 Other;
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MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCTGCCCTTCGCCTGGGACATC HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGC ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly ATGCGCTCCTCCAAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrValAspSerLysLeuAsp IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle AAGGTGAAGTTCATCGGCGTGAACTTCCCCCTCCGACGGCCCCGTGATGCAGAAGAAGAACC LysVallysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG cTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC ATCCACAAGGCCCTGAAGCTGAAGGACGGCCGCCACTACCTGGTGGAGTTCAAGTCCATC ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG (1-678)Length:
Matches:
Conservative:
Mismatches:
Indels: 678 225 0 0 100 300 180 60 120 40 60 20 240 80 220 200 540 180 160 420 140 360 120 999 600 480

661 CACCACCTGTTCCTG

675

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RESULT 9
ADDRESS PRESULT 9
ADD
                                                                                                   The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength control of the activity of a promoter, determining the age of a protein, converting the activity of a promoter, determining the age of a protein, controling a population of cells comprising a fluorescent timer protein are also useful for assessing gene carivity, an agent that modulates the activity of a promoter and in controling a population of cells comprising a fluorescent timer protein. The fluorescent timer proteins are also useful for assessing gene cellular differentiation, in response to a drug or other inducer of collular differentiation, in response to a drug or other inducer of compression during intracellular protein movement or translocation, controlled the activity of a regulatory element, for determining cell fate during development and organ remodelling, in spatial and temporal controlled to favore the activity of a regulatory element, for determining cell in distinguishing between newly formed and pre-existing structures, e.g. contending the proteins and accumulated proteins, and continuated proteins and extracellular matrix components. The fluorescent timer proteins may further be used to investigations where photobleaching techniques are employed, as detectable labels, as selectable markers, as biosensors in prokaryotic and eukaryotic cells, in protease cleavage assays, and as second messenger detectors. The nucleic acids can be used to generate transgenic, non-human plants or animals or site-specific gene modifications in cell lines. The present sequence is a DNA encoding conscious proteins fluorescent proteins.

Sequence is a DNA encoding generating fluorescent proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking
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protein age; anthozoa protein; drFP583; ds.
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            fluorescent protein variant; transcription induction detectic fluorescence energy resonance transfer; FRET; protein kinase; protein phosphatase; ion indicator; ds.
                                           Discosoma red fluorescent protein; DsRed; AB interface; AC interface; fluorescent protein variant; transcription induction detection;
                                                                                    Discosoma wild-type red fluorescent protein DNA #1.
                                                                                                                 18-DEC-2003
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                                                                                                                                                                                                                                    CACCACCTGTTCCTG
                                                                                                                                                                                                                                                                                            ATCACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGC
                                                                                                                                                                                                                                                                                                                                                    TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                            ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                         The invention describes a polynucleotide sequence (I) encoding a CC Discosoma red fluorescent protein (DBRed) variant having a reduced CC propensity to oligomerise, comprising amino acid substitutions at the AB CC and/or AC interfaces of the wild-type DBRed sequence (SI) comprising 225 cm and acids, given in the specification, where the substitutions result in reduced propensity of the DBRed variant to form tetramers. (I) is CC useful for detecting transcriptional activity by providing a host cells CC conatining a vector which comprises (I) operatively linked to an CC expression control sequence, and an unit to assay the variant fluorescent protein fluorescent protein fluorescent protein fluorescence, and assaying fluorescence of the variant fluorescent cC closalisation protein produced by (VII), where variant fluorescent protein fluorescence is indicative of transcriptional activity. A polynucleotide CC closalisation or trafficking of a polypeptide of interest. A polypeptide cC carget protein produced, where the target protein and amount of a CC target protein produced, where the target protein is fused to the marker, CC as a complement to or alternative for the green fluorescent protein or its spectral variant, for detecting induction of transcriptions, in CC which detects events as the function of the movement of fluorescent (FRET), CC which detects events as the function of the movement of fluorescent (CC interaction for ions and molecules such as Ca2+, Zn2+, for identifying the CC interaction of a first and second molecule, for determining whether a CC interaction of a first and second molecule, for determining whether a CC sample contains an enzyme or for otermining the pH of the sample. (I) is sample contains an enzyme or for determining the pH of the sample. (I) is sample contains an enzyme or for determining the pH of the sample. (I) is of an expression control sequence. This sequence encodes Discosoma wild-type red fluorescent protein.
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                                                                                                                US-10-006-922A-12 (1-225) x ADC24127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting transcriptional activity.
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24-MAY-2001; 2001US-00866538.
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                                                                                                                                                                                                                                                                                 Sequence 678
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CAMPBELL R E.
ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                     MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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                                                                 Hinuma
                                                                                                                                                                                   22-FEB-2002; 2002JP-00045728
23-JUL-2002; 2002JP-00213949
11-OCT-2002; 2002JP-00298237
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WPI; 2003-697654/66
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                                                                                                                                                                                                                                                                        The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New monomeric and dimeric Anthozoan fluorescent protein variants reduced propensity to oligomerize, and encoding polynucleotides, in molecular biology, e.g. in immunoassays or in tracking proteir
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                                                                                                                                                                                                DarkED encoding sequence.
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Score:

Percent Similarity:

Alignment Scores:

Sequence

678 BP; 205 A; 129

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178 G; 166 T; 0 U; 0 Other;

Pred. No.:

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The present invention relates to nucleic acid that encodes a rapidly commaturing chromo or fluorescent mutant of a Chidarian chromo- or fluorescent protein or its mutant. The protein is useful in applications convolving nucleic acid encoding a chromo- or fluorescent protein and is useful for producing a chromo and/or fluorescent protein which involves growing the cell, whereby the protein is expressed, and isolating the composition involving chromo- or fluorescent protein are useful in composition involving chromo- or fluorescent protein and is useful as pck primers, hybridization probes, etc. The expression cassettes are useful for synthesizing related proteins. The chromoproteins are useful as pck primers, hybridization probes, etc. The expression cassettes are useful as particular composition of matter e.g. food compositions, pharmaceuticals, commercies, living organisms, e.g., animals and plants. The chromoproteins compositions, pharmaceuticals, in applications, e.g. the production as selectable markers in recombinant to biological analytes of interest and as selectable markers in recombinant compositions, e.g. the production of transgenic cells and organisms. The fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in applications involving the automated screening of arrays of cells expressing fluorescent creporting groups by using microscopic imaging and electronic analysis, as second messenger detectors, and in fluorescence activated cell sorting applications and as in vivo marker in animals. The fluorescent proteins can also be used is assays to determine the phospholipid composition in biological composition in biological membranes and as a fluorescent timer. The present sequence represents the wild-type DeRED encoding sequence.
Novel nucleic acid encoding a rapidly maturing chromo- or fluorescent mutant of a Chidarian chromo- or fluorescent protein or its mutant, useful for applications involving chromo- or fluorescent proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 1; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for applications involving chromo-
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밁 δ 밁 á Best Local Similarity: Query Match: Ś S 밁 S US-10-006-922A-12 (1-225) x ADN33978 (1-678) 밁 片 181 121 61 41 61 21 AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120 HisasnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60 MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40 ASPTYTLYSLYSLEUSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100 ACGGTCAATGGGCACGAGTTTGAAATAGAAGGCGAAGGAGAGGGGAAGGCCATACGAAGGC ATGAGGTCTTCCAAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGCATGGAAGGA TIGICACCACAATITCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA 240 2.3e-140 1214.00 100.00% 100.00% 100.00% Conservative: Mismatches: Indels: Gaps: 678 0 225 0 0 180 120 60 80

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RESULT 14
AD136420
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 The invention relates to binding ligands (fluorobodies) with intrinsic fluorescence, which comprises green fluorescent protein (GFP) having heterologous binding sites. The binding ligand is useful for detecting the target molecule and is efficiently detects the target molecule. The
                                                                                                         Novel binding ligand with intrinsic fluorescence and comprising fluorescent protein having heterologous binding sites, useful for detecting target molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Discosoma
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DB; ADI36421.
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                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method of developing a sensor cell, for determining the activity of a target gene in the cell, which comprises providing a homogeneous population of cells, where each of the cells comprises a signal transduction detection system and introducing into the population of cells an isolated DNA construct comprising a promoter operatively linked to a targeting sequence. The method is useful in developing a sensor cell for determining the activity of a target gene in the cell. The sensor cell and the methods are useful in developing new and therapeutic drugs directed to the targets. The present sequence is a coding sequence shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; gene; enzyme; sensor cell; fluorescent protein; signal transduction detection system; promoter; targeting sequence; targeted drug.
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P-PSDB; ADM97769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 167-168; 234pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitney MA,
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                                                                                                    HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
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                                           LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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Search completed: January 12, 2006, 10:16:26 Job time : 485 Becs

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Result
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cgn2 1/USPTO epool p/US10006922/runat 10012006 162408 18933/app_query.fasta_1.391
-Q=/Cgn2 1/USPTO epool p/US1006922/runat 10012006 162408 18933/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1t6 -START=1 -END=-1 -MATRIX=b1osum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006922 @CGN 1 1 8010 @runat 10012006 162408 18933 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN INDEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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## ALIGNMENTS

RESULT 1

	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	DR987865/c LOCUS DEFINITION
Evolutionary Genomics  BYOS Joint Genome Institite  2800 Mitchell Drive, Walnut Creek, CA 94598, USA  Tel: 925-296-5823  Email: jaschwarz@lbl.gov  CDNA Library Preparation: DOE Joint Genome Institute:  CDNA Library Preparation: DOE Joint Genome Institute:  http://www.jgi.doe.gov  DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  DNA Sequencing: The suffix '.rev'  indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.	Unpublished (2005) Other ESTs: JGI AOSF1131.fwd Other ESTs: JGI AOSF1131.fwd	and Medina,M. Coral-Symbiodinium EST Project	Favilna; Favildae; Moncastraea.  1 (bases 1 to 556) Schwarz,J.A., Brokstein,P., Manohar,C., Coffroth,M.A., Szmant,A.	Montastraea faveolata Montastraea faveolata Montastraea faveolata Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;	DR987865 DR987865.1 GI:71782571 EST.	DR987865 556 bp mRNA linear EST 03-AUG-2005 JGI_AOSF1131.rev AOSF Montastraea faveolata adult colony Montastraea faveolata cDNA clone AOSF1131 3', mRNA sequence.

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US-10-006-922A-12 (1-225) x DR987865 (1-556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 GlyProLeuProPheAlaTrpAspIleLeuSerProGlnPheGlnTyrGlySerLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poly-T: A run of 14 or more T residues at the beginning of this sequence has been removed.

Small Insert: Based upon one or more sequencing reads of this clone where vector sequence was present at both ends, this clone has been determined to contain a cDNA insert on the order of 600-1000 bases. Plate: AOSF 0009 row: f column: 20
                                                                                                                                                                                                            HisTyrLeuValGluPheLysSerIleTyrMetAlaLysLysProValGlnLeuProGly 191
                                                                                                                                                                                                                                                                                                                                                                                                                                 AspGlyProValMetGlnLysLysThrMetGlyTrpGluAlaSerThrGluArgLeuTyr 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysTrpGluArgValMetAsnPheGluAspGlyGlyValValThrValThrGlnAspSer 111
GluGlnTyrGluArgThrGluGlyArg 220
                                                                                                       TyrTyrTyrValAspSerLysLeuAspIleThrSerHisAsnGluAspTyrThrIleVal
                                                                                                                                                                                                                                                                                                                            ProArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLysLeuLysAspGlyGly 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerLeuGlnAspGlyCysPheIleTyrLysValLysPheIleGlyValAsnPheProSer 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTGGGAACGTTGTATGACTTTCGAAGATGGAGGCATTTGCACCGTGTCAAACAACATC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCACCAAATACCCAAGAGACCTCCCAGACTATTTCAAGCAGTCGTTTCCTGCGGGGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCTCTCCCCTTTTGCTTACGATATCTTGACGACAGCATTCTCGTACGGCAACAGGGCA 437
                                                      TATCACTTTGTTGACCACCGAATTGAGATATTAAGTCATGACAAAGATTACAACAACGTG
                                                                                                                                                                 CATCACCGATGTAACTTCAGAAGTACTTACAAAGCCAAGAAGGATGTGGTGGTTGCCAGAA 149
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/lab host="ElectroMAX DH108"
/clone lib="AOSF Montastraea faveolata adult colony"
/clone lib="AOSF Montastraea faveolata adult colony"
/note="Vector: pDNR-LIB; Site_1: SfiI; Site_2: SfiI; The
library was prepared from total RNA using the Creator
SMART cDNA Library Construction Kit with the LD-PCR method
to amplify the cDNA. Amplified cDNA was digested with
sfiI, size selected for >400bp, and ligated into the
pDNR-LIB vector. WARNING: this library contains a small
percentage of cDNAs derived from the coral's symbiont,
Symbiodinium sp."
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/clone="AOSF1131"
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/mol_type="mRNA"
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RESULT 2
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  52 GlyProLeuProPheAlaTrpAspIleLeuSerProGlnPheGlnTyrGlySerLysVal
                                                                                  32 GluGlyGluGlyArgProTyrGluGlyHisAsnThrValLysLeuLysValThrLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: BST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
small Insert: Based upon one or more sequencing reads of this clone
where vector sequence was present at both ends, this clone has been
determined to contain a cDNA insert on the order of 600-1000 bases.
Plate: AOSF 0009 row: f column: 20
High quality sequence stop: 557.
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                                                  1 GACGGAGAAGGCAAGCCTTTCGAGGGAAAACACAGTATAAACCTTCCAAGTCCAAGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evolutionary Genomics
DOE Joint Genome Institite
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2005)
Other ESTs: JGI_AOSF1131.rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: jaschwarz@lbl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Schwarz, JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coral-Symbiodinium EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Cnidaria; A
Faviina; Faviidae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Montastraea faveolata
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JGI_AOSF1131.fwd AOSF Montastraea faveolata adult colony
Montastraea faveolata cDNA clone AOSF1131 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult colony"
/lab_host="ElectroMAX DH108"
/clone_lib="AOSF Montastraea faveolata adult colony"
/clone_lib="AOSF Montastraea faveolata adult colony"
/note="Vector: pDNR-LIB; Site_1: Sfil; Site_2: Sfil; The
library was prepared from total RNA using the Creator
SMART CDNA Library Construction Kit with the LD-PCR method
                                                                                                                                                                                                                                                                                                                                                                                                         to amplify the cDNA. Amplified cDNA was digested with SfiI, size selected for >400bp, and ligsted into the pDNR-LIB vector. WARNING: this library contains a small percentage of cDNAs derived from the coral's symbiont, Symbiodinium sp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Montastraea faveolata"
/mol_type="mRNA"
/db_xref="taxon:48498"
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RESULT 3
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BFL26_000139 Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMGp531) Branchiostoma floridae cDNA clone MPMGp531H0446 5', mRNA
(ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotide the grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: http://www.molgen.mpg.de/amphioxus/
                                                                                                                                                    laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: panopoulemolgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
                                                                                                                                                                                                                                                                                                                                      Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J. Herwig,R., Vingron,M. and Lehrach,H. Herwig,R., Vingron,M. and Lehrach,H. New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed anima
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Branchiostoma floridae
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                                                                                                                                                                                                                                                                       Contact: Panopoulou G
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                                                                                                                                                                                                                                                                                                                                     vertebrates using an amphioxus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLysLeuLysAspGlyGly 171
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                                                                                                                                                                                                                                                                                                                                                                                              Poustka, A.J.,
                                                                                                                                                                                                                                                                                                                                             animal
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          AlaLysLysProValGlnLeuProGlyTyrTyrTyrValAsp---SerLysLeuAspIle 201
                                                                                                                                                                                                                                                                                                                CATCGCGTGTTCGACTTTGAAGACGGAGGCAAGCTGTCCATCGAGTTTAAATACTCCTAC 358
                                                                                                                                                                                                                                                                                                                                                                               CCG---GACGGACCCTCGCCTTTCCAGGCCACCATGTTGGAAGGATCAGGGTATGCAGTC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTCTCCCTACTTGATGATCCCCCACCTCGGGTACGGGTACTACCAGTACCTCCCCTAC
                                                                           TyrLeuValGluPheLysSerIleTyr----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="MPMGp531H0446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Branchiostoma
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225.00
47.76%
30.85%
18.53%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAAGGGGGATGTG
Insert Length: 1 Std Error: 0.00
Seq primer: 5'-CCGGTCCGGAATTCCCCGGGT-3' pSport:
                                                                                                                                                                                                             Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de) PCR PRimers FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
floridae"
                                                                                                                        pSport3/86
                                                                                                                                                                                          ų
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/note="Vector: pSport1 (Gibco BRL); Site\_1: Sall, KpnI, EcoRI (5'); Site\_2: NotI, BamHI, HindIII (3'); OligodT primed and direcTionally cloned in pSport1 vector using NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a sall 5'-TCGACCCACGCGTCCG-3'adapters (Gibco BRL)." /clone lib="Amphioxus 26hr cDNA library (Name BFL26 or MPMGp531)" /dev stage="26 hrs (neurula stage)" /lab\_host="E.coli, XL1 blue" convention:

PheAlaTrpAspIleLeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHis 75

241

ProAlaAspIleProAspTyrLysLysLeuSerPheProGlu-----GlyPheLysTrp 93

GluarqValMetAsnPheGluaspGlyGlyValValThrValThrGlnAspSerSerLeu 113

GlnAspGlyCysPheIleTyrLysValLysPheIleGlyValAsnPheProSerAspGly

GAGGGTTCCCATATCAAGGCCGACATGAAGTTCACGGGAACCGGTTTCCCCTGAGGACGGG ProvalMetGlnLysLysThrMetGlyTrpGluAlaSer---ThrGluArgLeuTyrPro 133 152 418

ArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLysLeuLysAspGlyGlyHis 172 478

AACGACAACACCATCGTGGACAGCTTCGACTGGACTTACAACCTGCAGAATGGGAAGCGC 538 TACAAGGCCCAAGTGACGAGCCACTACATCTTCGGCAAGCCCTTTCCAGCCGATCTCATG ---Met 182

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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BW802012
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y.,
Expressed genes in Branchiostoma floridae
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 bp
BW802012 Amphioxus Branchiostoma
larva whole animal Branchiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
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BW802012.1 GI:66410228
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
              AAGTTCGAGGACGGCGGCGTCATGACCATCAAC--
                                                                                                                                                                               AATGACGGGACGCTGGAGACCAAGGTGCGGTCCACTAAGGGAGCC---CTGCCCTTCTCC
                                                                                                                                                                                              TyrGluĢļyHisAsnThrValLysLeuLysValThrLysGlyGlyFroLeuProPheAla
                                                                                                                                                                                                                                     ATGTTCGGCTCCATCAACGGCCACGAGTTCGACCTGGTGGGCGGTGGAAAAGGCGACCCG
                                                                                                                                                                                                                                                     MetGluGlyThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgPro
                                       AsnPheGluAspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCys 117
                                                                                                                         CCCGTGATCCTGGCCCCTAACCTGGGGTACGGGTACCACCAGTACCTGCCCTTCCCGGCC
                                                                                                                                                   TrpAspIleLeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAla
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81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole animal"
/dev_stage="larva"
/clone lib="Amphioxus Branchiostoma floridae
/clone library, larva whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:7739"
/clone="bblv023d19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Branchiostoma
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218.50
51.41%
36.62%
18.00%
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Matches:
Conservative:
Mismatches:
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floridae unpublished cDNA library,
floridae cDNA clone bblv023d19 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              unpublished
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BW736869
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Best Local Similarity:
                                                                                                                                                                                                         US-10-006-922A-12 (1-225) x BW736869
                                                                                                                                                                                                                                                            Query
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                                                                                                                                   493
                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tshini@genes.nig.ac.jp
If you want to have a cDNA clone for this EST or if you have ar
questions, please send an e-mail to Nori Satoh
(satch@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
(yutaka@ascidian.zool.kyoto-u.ac.jp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BW736869 Amphioxus Branchiostoma floridae unpublished cDNA library, egg whole animal Branchiostoma floridae cDNA clone bbeg003b16 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2005)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed genes in Branchiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Branchiostoma.
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BW736869
                                                                 GACCCGAACGCCGGCTCGCTGGTGACCACAGCGAAATCCACCAAG---GGTCCCCTGAAG
                                                                                              ArgProTyrGluGlyHisAsnThrValLysLeuLysValThrLysGlyGlyProLeuPro
TTCTCTCCCCACTTGATGATCCCCCACCTCGGGTACGGGTACTACCAGTACCTCCCCTAC
                             PheAlaTrpAspIleLeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PhelleTyr-----PhelleGlyValAsn
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J., Holland, L.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498
                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="egg"
/clone lib="Amphioxus Branchiostoma
cDNA library, egg whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="bbeg003b16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:7739"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Branchiostoma
                                                                                                                                                                                                                                            1.26e-15
218.50
48.28%
31.03%
18.00%
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                                                                                                                                                                                                           (1-646)
                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
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Indels:
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558
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                                                                                                                                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp
If you want to have a cDNA clone for this EST of questions, please send an e-mail to Nori Satoh (satch@asciddian.zool.kyoto-u.ac.jp) and its cc (yutaka@asciddian.zool.kyoto-u.ac.jp).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Expressed genes in Branchiostoma
Unpublished (2005)
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Branchiostoma floridae
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/dev stage="egg"
/clone lib="Amphioxus Branchiostoma
cDNA lībrary, egg whole animal"
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            1.64e-15
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Expressed genes in Branchiostoma floridae
Unpublished (2005)
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                                                                                                                                                                                                                                      Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                              Branchiostoma floridae (Plorida lancelet)
Branchiostoma floridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BW738638
BW738638.1 GI:66325268
                                                                                                    questions, please send an e-mail to Nori (satch@ascidian.zool.kyoto-u.ac.jp) and j (yutaka@ascidian.zool.kyoto-u.ac.jp).
Location/Qualifiers
                                                                                                                                                                       Email: tshini@genes.nig.ac.jp
If you want to have a cDNA clone for this EST or if you
                                                                                                                                                                                                        Tel: 81-559-81-6856
Fax: 81-559-81-6855
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                                 /organism="Branchiostoma
/mol_type="mRNA"
/db_xref="taxon:7739"
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tissue_type="whole animal"
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Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856
                                                                                  1 (bases 1 to 606)
Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y.,
Expressed genes in Branchiostoma floridae
Unpublished (2005)
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostoma.
                                                                                                                                                                                             Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
                                                                                                                                                                                                                                                                   mRNA sequence.
BW741633
                                                                       Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                BW741633.1 GI:66328281
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/clone lib="Amphioxus Branchiostoma floridae unpublished
cDNA lībrary, egg whole animal"
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mRNA sequence.
BI379468
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EST.
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                                                             BI379468 637 bp mRNA linear EST 26-AUG-200: BFLG1 001099 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGp498) Branchiostoma floridae cDNA clone MPMGp49801918 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp
If you want to have a cDNA clone for this Ex
questions, please send an e-mail to Nori Sat
(satch@ascidian.zool.kyoto-u.ac.jp) and its
(yutaka@ascidian.zool.kyoto-u.ac.jp).
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CACCGCGTGTTTGATTTCGAAGACGGAGGCAAGCTGTCCATCGAGTTTAAGTACTCCTAC 362
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/mol_type="mRNA"
/db_xref="taxon:7739"
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/clone_lib="Amphioxus Branchiostoma
cDNA lībrary, egg whole animal"
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/tissue_type="whole animal"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 Smer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at http://www.molgen.mpg.de/amphioxus/Clones and filers are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de)
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Branchiostoma floridae
                                                                                                  Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J., Herwig, R., Vingron, M. and Lehrach, H. New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 1200 Std Error: 0.00 Seg primer: 5'-CCGGTCCGGAATTCCCGGGT-3' High quality sequence stop: 637.
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Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13FSP)
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: panopoul@molgen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Panopoulou G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 13 (6A), 1056-1066 (2003)
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                                             GlyArgProTyrGluGlyHisAsnThrValLysLeuLysValThrLysGlyGlyProLeu 54
                                                                                                                                  LysValArgMetGluGlyThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGlu 34
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+49 30 8413 1128
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/dev stage="5-6 hrs (gastrula stage)"
/lab_host="E.coli, XLI blue"
/clone lib="Amphioxus 5-6 hrs cDNA library (Name convention: BFIG or MPMGp498)"
/note="Vector: pSportl; Site 1: Sall, KpnI, EcoRI (5')
/note="Vector: pSportl; Site 1: Sall, KpnI, EcoRI (5')
/incte="toti, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSportl vector using a NotI (5'-pGACTAGTTCTAGATCGCGGGGGGGCGCCC (7)15-3' and a Sall
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                                                                                                                                   The library was characterised by oligonucleotide fingerprinting (ONPP) to reduce sequencing redundancy. According to the ONPP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: http://www.molgen.mpg.de/amphioxus/Clones and filters are distributed via the Resource Center/Primary companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J
Herwig,R., Vingron,M. and Lehrach,H.
New evidence for genome-wide duplications at the origin of
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BFL26 002620 Amphioxus 26hr cDNA library (Name convention: BFL26 o
MPMGp531) Branchiostoma floridae cDNA clone MPMGp531N0767 5', mRNA
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Ihnestr.63-73, D-14195 Berlin, Germany
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Branchiostoma floridae
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                  Contact: Panopoulou G
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                                                                                            Database of the German Genome Project (http://www.rzpd.de)
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+49 30 8413 1128
1: panopoul@molgen.mpg.de
5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
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                                                    (M13FSP)
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             BI386699.1
                                           BI386699
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                                                                                                                                                                                                                                                                                                                                                                  TyrLeuValGluPheLysSerIleTyrMetAlaLysLysPro 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCGCGTGTTCGACTTTGAAGACGGAGGCAAGCTGTCCATCGAGTTTAAGTACTCCTAC 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pSport1 (Gibco BRL); Site 1: Sall, KpnI, EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCC (T)15-3' and a Sall 5'- TCGACCCACGCGTCCG-1'adartee (7')
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/dev stage="26 hrs (neurula stage)"
/lab_host="E.coli, XLi blue"
/clone lib="Amphioxus 26hr cDNA library (Name convention:
/sto-"Yosto", Colory: Colory (Name convention:
/sto-"Yosto", Colory: C
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/db_xref="taxon:7739"
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                    US-10-006-922A-12 (1-225) x BI386699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
141 GACCCGAACGCCGGCTCGCTGGTGACCACAGCGAAATCCACCAAG---GGTCCCCTGAAG 197
                                        36 ArgProTyrGluGlyHisAsnThrValLysLeuLysValThrLysGlyGlyProLeuPro
                                                                                                               81 ATCCACCTTCACGGCTCCATCAACGGCCACGAGTTCGACATGGTGGGGGGGAAAAAGGC 140
                                                                                                                                                                      16 ValArgMetGluGlyThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: http://www.molgen.mpg.de/amphioxus/clones and filters are distributed via the Resource Center/Primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J., Herwig, R., Vingron, M. and Lehrach, H. New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13RSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database of the German Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Panopoulou G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 13 (6A), 1056-1066 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branchiostoma.

1 (bases 1 to 643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12799346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="MPMGp531L1370"
/tissue_type="whole embryo"
/dev_stage="26 hrs (neurula stage)"
/lab_host="R_coli, XL1 blue"
/clone_lib="Amphioxus_26hr_cDNA_library (Name_BFL26 or MPMGp531)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pSport1 (Gibco BRL); Site_1: SalI, KpnI, EcoRI (5'); Site_2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (7)15-3' and a SalI 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Branchiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           6.69e-15
212.50
47.87%
29.79%
17.50%
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                                                                                                                                                                                                                                       (1-643)
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Matches:
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34
87
11
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RESULT 12
BI382638
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DEFINITION
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KEYWORDS
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
Contact: Panopoulou G

Contact: Panopoulou G

Contact: Adopt.Lehrach

Max-Planck-Institut fuer Molekulare Genetik

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Tel: +49 30 8413 1235

Fax: +49 30 8413 1235

Fmail: panopoul@molgen mpg.de

The library was characterised by oligonucleotide fingerprinting

(ONFP) to reduce sequencing redundancy. According to the ONFP

procedure, clones giving the same hybridisation pattern with a

battery of 200 8mer oligonucleotides are grouped into clusters. One

clone per cluster is selected for sequencing. The size of each

cluster is an indicator of the frequency of a transcript in the

analysed library. The cluster size as well the coordinates of the

rest of the clones assigned to the same fingerprint cluster as the

clone from which the above EST is generated is available at the

amphioxus project site at: http://www.molgen.mpg.de/amphioxus/

Clones and filers are distributed via the Resource Center/Primary

Database of the German Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI382638 675 bp mRNA linear EST 26-AUG-2
BFLG2 000815 Amphioxus 5-6 hrs cDNA library (Name convention: BF
or MFMGp498) Branchiostoma floridae cDNA clone MFMGp498F0258 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J
Herwig,R., Vingron,M. and Lehrach,H.
New evidence for genome-wide duplications at the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 13 (6A), 1056-1066 (2003)
12799346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vertebrates using an amphioxus gene set and completed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Branchiostoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProAlaAspIleProAspTyrLysLysLeuSerPheProGlu-----GlyPheLysTrp 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCTCCCTACTTGATGATCCCCCACCTCGGGTACGGGTACTACCAGTACCTCCCCTAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACAACAACACCATCGTGGACAGCTTCGACTGGAGTTACAACCTGCAGAATGGGAAGCGC 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLysLeuLysAspGlyGlyHis 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProvalMetGlnLysLysThrMetGlyTrpGluAlaSer---ThrGluArgLeuTyrPro 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCG---GACGGACCCTCGCCTTTCCAGGCCTCCATGTTGGAAGGATCGGGGTATGCAGTC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAAGCAGCCGGTCTTCGTGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrLeuValGluPheLysSerIleTyrMetAlaLysLysPro--------
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                               464
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                                                                                                                                                                                                                                                                                     404
                                                                                                                                                                                                                                                                                                                                                       344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
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                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                               76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRIMERS
FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (1 PORWARD: 5' CCTATTACGCCCACTTGCGCAAAGGGGGATGTG 3' Insert Length: 1 Std Error: 0.00
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 675
                                                                                                                                                                                                                                                                                                                                                                                      GluarqValMetAsnPheGluaspGlyGlyValValThrValThrGlnAspSerSerLeu 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTCCCCCTACTTGATGATCCCCCACCTCGGGTACGGGTACTACCAGTACCTCCCCTAC
                                                                                                                                                                                                                                                                                                                  GlnAspGlyCysPheIleTyrLysValLysPheIleGlyValAsnPheProSerAspGly 133
                                                                                                                                                                                                                                                                                                                                                         PheAlaTrpAspIleLeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHis 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgProTyrGluGlyHisAsnThrValLysLeuLysValThrLysGlyGlyProLeuPro 55
                                                                                                                                                                        ArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLysLeuLysAspGlyGlyHis 172
                                                                                                                                                                                                                                              ProValMetGlnLysLysThrMetGlyTrpGluAlaSer---ThrGluArgLeuTyrPro
                                                                                                                                                                                                                                                                                   GAGGGTTCCCATATCAAGGCCGACATGAAGCTGATGGGAAGCGGTTTCCCTGACGACGGC
                                                                       TACAAGGCCCGAGTGTCNAGCCACTACATCTTCGACAAGCCC
                                                                                                    TyrLeuValGluPheLysSerIleTyrMetAlaLysLysPro 186
                                                                                                                                           AACAACAACACCATCGTGGACAGCTTCGACTGGAGTTACAACCTGCAGAATGGGAAGCGC
                                                                                                                                                                                                               CCAGTCATGACCAGCCAGATTGTCGACCAGGACGGCTGCGTGTCCCAAGAAGACGTATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                             CCG---GACGGACCCTCGCCTTTCCAGGTCTCCATGTTGGAAGGATCGGGGTATGCAGTC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProAlaAspIleProAspTyrLysLysLeuSerPheProGlu-----GlyPheLysTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole embryo"
/dev stage="5-6 hrs (gastrula stage)"
/dev stage="5-6 hrs (gastrula stage)"
/lab_host="Bcooli, XLi blue"
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name
convention: BFLG or MPMG9498)"
/note="Vector: pSportl, Site_1: Sall, KpnI, EcoRI (5');
Site_2: NotI, BamHI, HindIII 3'); OligodT primed and
directionally cloned in pSportl vector using a NotI
(5'-pGACTGGTTCTAGATCGCAGCGGCCCC (T)15-3' and a Sall 5'
TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:7739"
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Fax: 81-559-81-6855
Email: tshini.genes.nig.ac.jp.
Location/Qualifiers
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Center For Genetic Resource Information
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Yu, J., Holland, L.Z., Shin-i, T., Kohara, Y.,
Expressed genes in Branchiostoma floridae
Unpublished (2005)
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Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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                                                                                        ProValMetGlnLysLysThrMetGlyTrpGluAlaSer---ThrGluArgLeuTyrPro
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/mol type="mRNA"
/db xref="taxon:7739"
/clone="bbne135]09"
/tissue_type="whole animal"
/dev_stage="neurula"
/dev_stage="neurula"
/clone_lib="Amphioxus Branchiostoma flooring lib="Amphioxus Branchiostoma flooring lib="animal"
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                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
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Expressed genes in Branchiostoma
Unpublished (2005)
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                                   TACCGCGTGTTCGACTTTGAAGACGGAGGCAAGCTGACTACCGAGTTTAAGTACTCCTAC
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                                                                       GluArgValMetAsnPheGluAspGlyGlyValValThrValThrGlnAspSerSerLeu 113
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                                                                                                           GACGGACCCTCGCCTTTCCAGACCTCCATGTTGGAAGGATCGGGGTATGCAGTC 293
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/tissue_type="whole animal"
/dev_stage="neurula"
/clone_lib="Amphioxus Branchiostoma
/clone_lib="Amphioxus Branchiostoma
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DKFZp434P092 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434P092 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                  Ingolstsedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Canc Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of German Genome Project.
                                                                                                                                                                                                                                                                                                                               No s1 sequence available.
This clone (DKPZp634P092) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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Unpublished (1999)
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Anasorge, W., Benes, V., Krieger, S., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                            GlnLeuProGlyTyrTyrTyrValAspSerLysLeuAspIleThr-----SerHis 204
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                                                                                                                                                                                                                                                                                                                                                                            ProAlaAspIlePro-----AspTyrLysLysLeuSerPheProGluGlyPheLysTrp 93
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                                                                                                                                                            AspGlyValLeuLysGlyGluIleHisLysAlaLeuLysLeuLys------
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                          AsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArgHisHis 222
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Search completed: January 12, 2006, 12:23:29 Job time : 3750 secs

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Title:
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and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Sequence 11, Appli
Sequence 1, Appli
Sequence 45, Appli
Sequence 1, Appli
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Sequence 2, Appli
Sequence 2, Appli
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equence 30	equence 21	equence 31	გ	equence 24	equence 24	equence 2,		equence 23	equence 26	equence 23	equence 19	equence 19	equence 1,	equence 1,	equence 1,	equence 3,	equence 6, Appi	equence 1, Appl	e 1, Appi	equence 31, App	equence 31, App	equence 30, App	equence 30,	equence 2, Appl	equence 2, Appl	equence 3,	nce 3,	equence 1,	equence 1,	equence 4,	equence 15,	equence 64,	equence 64,	quence 64, App	equence 15, Ap

## ALIGNMENTS

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Patent No. 5342...

PATELICANT: TSién, ROGET Y.

APPLICANT: TSIÉN, ROGET Y.

APPLICANT: TSIÉN, ROGET Y.

APPLICANT: GONZALEZ, III, JESUS E.

APPLICANT: GONZALEZ, III, JESUS E.

APPLICANT: GONZALEZ, III, JESUS E.

TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY

TITLE OF INVENTION: OPTICAL METHODS

FILE REFERENCE: REGEN1290-4

CURRENT FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 08/765,860

PRIOR FILING DATE: 1999-05-08

PRIOR FILING DATE: 1999-05-08

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR APPLICATION NUMBER: PCT/US96/09652

PRIOR APPLICATION NUMBER: PCT/US96/09652
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US-09-459-956-6
Query Match:
DB:
                                     Percent Similarity:
Best Local Similarity:
                                                                             Score:
                                                                                             Alignment Scores: Pred. No.:
                                                                                                                                                       US-09-459-956-6
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                         TYPE: DNA
ORGANISM: Discosoma
                                                                                                                                                                                                               LENGTH: 678
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Conservative:
Mismatches:
Indels:
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APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: CAMPBEL, ROBERT
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PRO
FILE REFERENCE: REGEN1530-2
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 859
TYPE: DNA
ORGANISM: Discosoma sp.
FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(731)
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                                                                                                                                                                                                                                                    Sequence 11, Application Patent No. 6852849
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Pred. No.:
    GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGET
APPLICANT: TING, Alice
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS
FILE REFERENCE: REGEN1550
CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 42
                                                                                                                                           Sequence 11, Application US/09865291 Patent No. 6900304
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LENGTH: 859

TYPE: DNA

ORGANISM: Discosoma sp
FEATURE:
NAME/KEY: CDS
LOCATION: (54)...(731)
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RESULT 4
US-10-152-296-1
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; Patent No. 6723537
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APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Directed Evolution of Protein:
FILE REFERENCE: 021044-000110US
CURRENT APPLICATION NUMBER: US/10/152,296
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION UNMER: US 60/291,871
PRIOR PILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 2
SOPTWARE: Patentin Ver. 2.1
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NAME/KEY: CDS
LOCATION: (1)..(723)
OTHER INFORMATION: DERED
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Best Local Similarity:
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APPLICANT: BLAW, TERESA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUI
TITLE OF INVENTION: VECTOR PIGGYBAC
FILE REFERENCE: 835910-92098
CURRENT APPLICATION NUMBER: US/10/001,189
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
ROTETION SEQ ID NOS: 70
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SEQ ID NO 45
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Patent No. 6962810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                      3034 ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGC
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                                                                                                                                                                                                                                                                                                         LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                              AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                    AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                                                           LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                                                CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCTGCCCTTCGCCTGGGACATC
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SEQ ID NO 5
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APPLICANT: TSien, Roger Y.

APPLICANT: GONZALEZ, III, Jesus E.

APPLICANT: GONZALEZ, III, Jesus E.

APPLICANT: GONZALEZ, III, Jesus E.

APPLICATION: DETECTION OF TRANSMEMBRANE POTENTIALS BY

TITLE OF INVENTION: OPTICAL METHODS

FILE REFERENCE: REGEN1290-4

CURRENT APPLICATION NUMBER: US/09/459,956

CURRENT FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 08/765,860

PRIOR FILING DATE: 1999-05-06

PRIOR FILING DATE: 1999-06-07

PRIOR APPLICATION NUMBER: PCT/US96/09652

PRIOR FILING DATE: 1996-06-06

NUMBER OF SEQ ID NOS: 22
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US-09-459-956-5
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                                                                       61 LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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                                                                                                                                                                                                 ; LENGTH: 860
; TYPE: DNA
; ORGANISM: Montastrea
US-10-244-779-1
                                                                                                                                                                                                                                                                                           APPLICANT: Gorbunov, Maxim
APPLICANT: Wyman, Kevin
APPLICANT: Chen, Yi-Bu
APPLICANT: Chen, Yi-Bu
TITLE OF INVENTION: mcFP Encoding Nucleic Acids,
TITLE OF INVENTION: Polypeptides, Antibodies and M
FILE REFERENCE: Rut 00-0023US
CURRENT APPLICATION NUMBER: US/10/244,779
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/322,189
PRIOR FILING DATE: 2001-09-14
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                                                           US-10-006-922A-12 (1-225) x US-10-244-779-1 (1-860)
                                                                                                                                Percent Similarity:
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                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                  Local Similarity:
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           138
        Kun, Yi
Gorbunov, Maxim
"man, Kevin
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US-09-459-956-7
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                                                                                                        ; LENGTH: 801
; TYPE: DNA
; ORGANISM: Clavularia
US-09-459-956-7
                                                        Score:
                                                                   Pred. No.:
                                                                               Alignment Scores
                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/76
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/48
PRIOR APPLICATION NUMBER: 095-06-07
PRIOR APPLICATION NUMBER: PCT/UI
PRIOR APPLICATION NUMBER: PCT/UI
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows V
                                                                                                                                                                                                                                                                                                                                                                                           sequence 7, Application Patent No. 6342379
                                                                                                                                                               SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Tsien, Roger Y.
APPLICANT: Gonzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE
TITLE OF INVENTION: OPTICAL METHODS
                                                                                                                                                                                                                                                                                     FILE REFERENCE: REGEN1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13
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Matches:
Conservative:
  Gaps:
                  Mismatches:
Indels:
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APPLICANT: Tsien, Roger Y.

APPLICANT: Gonzalez, III, Jesus E.

APPLICANT: Gonzalez, III, Jesus E.

APPLICANT: Gonzalez, III, Jesus E.

APPLICANT: DETECTION OF TRANSMEMBRANE POTENTIALS BY

TITLE OF INVENTION: OPTICAL METHODS

FILE REPERENCE: REGEN1290-4

CURRENT APPLICATION NUMBER: US/09/459,956

CURRENT FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 08/765,860

PRIOR APPLICATION NUMBER: 08/81,977

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1996-06-06

NUMBER OF SEQ ID NOS: 22

PRIOR FILING DATE: 1996-06-06
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SOFTWARE: Fa
SEQ ID NO 2
LENGTH: 690
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Sequence 2, Application US/09459956
Patent No. 6342379
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US-09-609-161B-15
; Sequence 15, Application US/09609161B
; Patent No. 6436682
; Patent No. 6436682
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Best Local Similarity:
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; ORGANISM: Anemonia
US-09-459-956-2
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APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS,
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE I
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
CURRENT FILLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/277,716
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PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.0
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LOCATION: (259)..(975)
OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
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ORGANISM: Renilla mulleri
FEATURE:
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CAACATCGTTTGGAAAAGACT---TACGTAGAAGACGGGGGGTTCGTTGAACAGCATGAG
                      AspSerLysLeuAspIleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGlu 215
                                                ATGAAAACATTAATGAAGTCGAAAGGTGTAGTAAAGGAGTTTCCTTCGTATCATTTATT
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US-10-006-922A-12 (1-225) x US-09-626-581D-64 (1-1079)
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APPLICANT: Anderson
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TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
FILE REFERENCE: A-66900-3/RMS
CURRENT APPLICATION NUMBER: US/99/626,581D
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/415,765
PRIOR APPLICATION NUMBER: 09/415,765
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LOCATION: (259)...
OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Renilla muelleri
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; FEATURE:
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; LOCATION: (259)..(9
; OTHER INFORMATION:
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APPLICANT: Anderson, David
APPLICANT: Anderson, David
TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
FILE REFERENCE: A66900-1/RMS/ANS
CURRENT APPLICATION NUMBER: U8/09/415,765B
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
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Patent No. 654863
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ORGANISM: Renilla muelleri
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      GlnLysLysThrMetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyVal
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Best Local Similarity:
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US-09-626-580C-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/626,580C CURRENT FILING DATE: 2000-07-27 PRIOR APPLICATION NUMBER: US 09/415,765 PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: FUSIONS OF SCAFFOLD PROTEINS
FILE REFERENCE: A-66900-2/RMS/AMS
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PRIOR FILING DATE: 1998-10-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (259)...
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      MetAsnPheGluAspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGly 116
                                            AlaAspIleProAspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgVal 96
                                                                                                                                                  AlaTrpAspIleLeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisPro 76
                                                                                                                                                                                                    ATTTTATTCGGCAATCAACTGGTTCAGATTCGTGTCACGAAAGGGGCCCCACTGCCTTTT
                                                                                                                                                                                                                        ProTyrGluGlyHisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPhe 56
                                                                                                                                                                                                                                                                                AATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGGAGGGTTGCGGCAAAGGGAAT 375
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Pred. No.:
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US-09-277-716-15
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Sequence 15, App.
No. 623210
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                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Renilla mulleri
PEATURE:
NAME/KEY: CDS
LOCATION: (259)..(975)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING CURRENT APPLICATION NUMBER: US/09/277,716A

CURRENT FILING DATE: 1999-03-26

EARLIER PILING DATE: 1998-10-01

EARLIER FILING DATE: 1998-10-01

EARLIER APPLICATION NUMBER: 60/089,367

EARLIER APPLICATION NUMBER: 60/089,367

EARLIER APPLICATION NUMBER: 60/089,367

EARLIER FILING DATE: 1998-03-27

EARLIER FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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                                                AATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGGAGGGTTGCGGCAAAGGGAAT
                                                                         ArgMetGluGlyThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArg
                                                                                                                                        ArgSerSerLysAsnValIleLys------GluPheMetArgPheLysVal
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ProTyrGluGlyHisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPhe
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Patent No. 6342379
GENERAL INFORMATION:
APPLICANT: Teien, Roger Y.
APPLICANT: Gonzalez, III, Jesus E
                                                                                                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
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                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Zoanthus
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APPLICANT: GONZALEZ, III, JESUS E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE
TITLE OF INVENTION: OPTICAL METHODS
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                                   MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly 20
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ATGGCTCATTCAAAGCACGGTCTAAAAAGAAGAAATGACAATGAAATACCACATGGAAGGG
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Search completed: January 12, 2006, 12:26:40 Job time : 185 secs
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                                                                                                                                                                                                                                                                                                                                    LeuLysGlyGluIleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGlu 176
                                                                                                                                             LysThrMetGlyTrpGluAlaSerThrGluArgLeu-----TyrProArgAspGlyVal 156
                                                                                                                                                                                                  ABDTYTLYBLYBLEUSErPheProGluGlyPheLy8TrpGluArgValMetAsnPheGlu 100
                                 CAGCATAAGCTC 612
                                                                                 PheLysSerIleTyrMetAlaLysLys---ProValGlnLeuProGlyTyrTyrTyrVal 195
                                                                                                                                                                                                                                                                    TIGTCAGCTGGCTTTAAGTACGGAGACAGGATTTTCACTGAATATCCTCAAGACATAGTA 240
                                                                 TTCGACACAGTTTACAAAGCCAAAGTCTGTGCCAAGTAAGATGCCGGAGTGGCACTTCATC 600
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Result
No.
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-MODEL-frame+_p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_8pool_p/US10006922/runat_10012006_162409_18977/app_query.fasta_1.391
-DB=PublIshed_App_ications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -ENN=-1
-MATRIX-blosum62 -TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext
-THR_MAX=100 -THR_MIN=0 -MAXLEN=200000000
-USER-US10006922 @CGN 1 1_1549 @runat_10012006_162409_18977 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11E_PUBCOMB.seq:*
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Sequence 4, Appli	equence 3,	equence 2, Appl	e 3, Appl	equence 4, Appl	equence 20, App	equence 20,	equence 45	equence 46	Sequence 2	equence 16, Appl	e 29	equence 75	equence 51	equence 1,	equence 1,	equence 12, App	H	23	ıω	8, Appl	Sequence 23, Appl	3, Appl	35, Apr	3, Appı	equence 11, App	equence 11, App	Sequence 12, Appl	equence 11, App	equence 11,	Ф		equence 2,	equence 1, Appl	equence 27, App	equence 21, App	equence 5,	equence 6, Appl	

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## ALIGNMENTS

RESULT 1

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ADPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: TSIEN, ROSER

JOS-09-567-772-6

JOS-09-67-772-6

JOS-09-67-772-6

JOS-09-67-772-6

ALIGNMENT STIENG DATE: 1995-10-19

JOS-09-967-772-6

ALIGNMENT SCOTES: 6.83e-143

Length: 678

Length: 678

Length: 678

Length: 678

Length: 678

Alignment Scotes: 6.83e-143

Length: 678

Scotes: 1214.00

Matches: 225
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Sequence 11, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey A
APPLICANT: Lukyanov, Sergey A
APPLICANT: Lukyanov, Sergey A
APPLICANT: Lukhasi V.
APPLICANT: Lukhasi V.
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
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US-10-006-922-11
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PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR PILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.
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; ORGANISM: Discosoma
US-10-006-922-11
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                                                                     IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
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                                                                                                                 TACATGGCAAAGAAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAAACTGGAT
                                                                                                                                 TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
                                                                                                                                                                               ATTCATAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAAGTATT
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APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushevich, Yuriy
APPLICANT: Yanushevich, Yuriy
APPLICANT: Yanushevich, Yuriy
APPLICANT: Fradkov, Alexandr
APPLICANT: Fradkov, Arcady
ITITE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
ITITE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067
CURRENT APPLICATION NUMBER: 10/006,922
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
SEQ ID NO 7
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ORGANISM: Discosoma
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IleH16Ly8AlaLeuLy8LeuLy8AspGlyGlyH16TyrLeuValGluPheLy8SerIle
                                                                   MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                              AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTGATGCAGAAGAAGACC
                                                                                                                                 LygValLygPheIleGlyValAgnPheProSerAspGlyProValMetGlnLygLygThr
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APPLICANT: TBien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAP
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SEQ ID NO 2
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LOCATION: (1)...(678)
OTHER INFORMATION: wild-type DsRed
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ORGANISM: Discosoma sp
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AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                       LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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                                                     AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                  TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA
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CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR PELLING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PastSEQ for Windows Version 4.0
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US-10-315-920-1
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Publication No. US20030175809A1
GENERAL INFORMATION:
APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Terskikh, Alexey
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 678
                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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DB:
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ORGANISM: Discosoma sp.
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APPLICANT: Zeytun, Ahmet
APPLICANT: Waldo, Geoffrey
APPLICANT: Waldo, Geoffrey
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Fluorobodies: Binding Ligands With Int
ITILE OF INVENTION: Fluorescence
FILE REFERENCE: 021362-000600US
CURRENT APPLICATION NUMBER: US/10/132,067
CURRENT FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                     OTHER INFORMATION: red flu; FEATURE; NAME/KEY: CDS; LOCATION: (1)...(678); OTHER INFORMATION: dsred US-10-132-067-3
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Sequence 6, Application US/10335517

Publication No. US20030207248A1

GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFC APPLICANT: TSIEN, ROGET
APPLICANT: TSIEN, ROGET
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POT FILE REFERENCE: REGEN1290-5

CURRENT APPLICATION NUMBER: US/09/967,772
PRIOR APPLICATION NUMBER: US/09/967,772
PRIOR APPLICATION NUMBER: US 09/459,956
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR FILING DATE: 1996-12-19
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR FILING DATE: 1996-06-06
PRIOR PILING DATE: 1996-06-06
PRIOR PILING DATE: 1995-06-06
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        RESULT 8
US-10-314-288-6
; Sequence 6, Application US/10334288
; Publication No. US20040002123A1
; GENERAL INFORMATION:
; APPLICANT: THE REGERTS OF THE UNIVERSITY
; APPLICANT: TSIEN, Roger
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp "red
US-10-335-517-6
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1 CACCATCTGTTCCTT
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APPLICANT: GONZALEZ, Jesus
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REGENIZ90-5
CURRENT APPLICATION NUMBER: US/10/334,288
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US/967,772
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 199-12-13
PRIOR APPLICATION NUMBER: US/96/55,860
PRIOR FILING DATE: 199-12-13
PRIOR APPLICATION NUMBER: US/96/09652
PRIOR FILING DATE: 1996-12-19
PRIOR APPLICATION NUMBER: US/96/09652
PRIOR FILING DATE: 1996-06-06
PRIOR FILING DATE: 1996-06-06
PRIOR APPLICATION NUMBER: US/98/09652
PRIOR FILING DATE: 1996-06-07
NUMBER OF SEQ ID NOS: 22
SOFTMARE: PatentIN version 3.0
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TYPE: DNA
ORGANISM: Discosoma
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Sequence 5, Application US/10311030
; Publication No. US20040171107A1
; GENERAL INFORMATION:
   APPLICANT: Nelson, David
   APPLICANT: Tsien, Roger
   TITLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS
   FILE REFERENCE: 15916-032US1
   CURRENT FILING DATE: 2002-12-10
   PRIOR APPLICATION NUMBER: US/10/311,030
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US01/04625
; PRIOR APPLICATION NUMBER: US 60/184,732
; PRIOR APPLICATION NUMBER: US 60/184,732
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 678
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                 MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
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Sequence 21, Application US/10656029

Publication No. US20050003367A1

GENERAL INFORMATION:
APPLICANT: VERTEX PHARMACEUTICALS INC.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RAPID DEVELOPMENT OF TITLE OF INVENTION: SCREENING ASSAYS
FILE REFERENCE: VPI/O2-143MO2
CURRENT APPLICATION NUMBER: US/10/656,029
CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: 60/408,297
PRIOR APPLICATION NUMBER: 60/408,297
PRIOR PILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 86
SOPTWARE: Patentin version 3.2
SEQ ID NO 21
LENGTH: 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; HAME/KEY: CDS
; LOCATION: (1)..(678)
; OTHER INFORMATION: fluor
US-10-656-029-21
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Best Local Similarity:
Query Match:
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US-10-656-029-21
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                                                                                                                   LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                   CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGACCTTTGCCATTTGCTTGGGATATT
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AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                   AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA
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TITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: P03-0006PCT
CURRENT APPLICATION NUMBER: US/10/505,486
CURRENT FILING DATE: 2004-08-20
FRIOR APPLICATION NUMBER: JP 2002-45728
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: JP 2002-213949
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: JP 2002-213949
PRIOR APPLICATION NUMBER: JP 2002-298237
PRIOR APPLICATION NUMBER: JP 2002-298237
PRIOR FILLING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 233
SEQ ID NO 27
TENTUM. 678
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US-10-505-486-27
ig-10-505-486-27
; Sequence 27, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Discosoma
US-10-505-486-27
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     {\tt LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro}
                                         CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGGACCTTTGCCATTTGCTTGGGATATT
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	Qy 1 MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly	S-10-006-922A-12 (1-225) x	Alignment Scores:  Fred. No.:  6.83e-143  Score:  1214.00  Percent Similarity:  100.00\$  Best Local Similarity:  100.00\$  Query Match:  9  Gaps:  678  Conservative:  0  Mismatches:  0  Gaps:  0  Gaps:	PRIOR FILING DATE: 2001-12-19 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1 LENGTH: 678 TYPE: DNA ORGANISM: Discosoma US-10-844-064A-1	FILE REFERENCE: 092234-9006  CURRENT APPLICATION NUMBER: US/10/844,064A  CURRENT FILING DATE: 2004-05-11  PRIOR APPLICATION NUMBER: PCT/US02/40539  PRIOR PRIOR FILING DATE: 2002-12-18  PRIOR PRIOR FILING DATE: 2002-12-18	GENERAL INFORMATION:  APPLICANT: Bevis, Brooke  APPLICANT: Glick, Benjamin  TITLE OF INVENTION: RAPIDLY MATURING FLUORESCENT PROTEINS AND METHODS	RESULT 12 US-10-844-064A-1 US-10-844-064A-1 ; Sequence 1, Application US/10844064A ; Depart on No. 113200501499441	Oy 221 HisHisLeuPheLeu 225	Oy 201 IleThrSerHisasnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyAr	QY 181 TyrMetAlaLysLysBroValGlnLeuProGlyTyrTyrValAspSerLysLeuAsp	Oy 161 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle	OY 141 MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGl	Qy 121 LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr	Qy 101 AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTy	Qy 81 AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu	Db 181 TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA
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Sequence 66, Application US/09999745

Patent No. US20020157120A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THILE, ROGET Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
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; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(731)
US-09-999-745-66
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PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
SEQ ID NO 66
LENGTH: 859
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                                                              HisHisLeuPheLeu 225
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Publication No. US20030032088A1

GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROFILE REFERENCE: REGEN1530-2
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-5-24
INUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
ALENCTH: 859
TYPE: DNA
ORGANISM: Discosoma sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (54)...(731)
US-09-866-538-11
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Result
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-MODEL-frame+ p2n.model -DEV=xlp
-Q-(cgn2 1)(USPTO gpool p.)(USJ0006922/runat 10012006 162410 19008/app query.fasta 1.391
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPEX/T=0 -UNITS=blits -STATT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DORALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXELN=200000000 -USER=US10006922 @CGN 1 1 184 @TUNAt 10011006 162410 19008
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=10 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

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4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-218-880-2

US-10-209-208-3

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US-11-218-880-3

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US-10-655-872-7
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Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
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## ALIGNMENTS

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US-10-209-208-2
US-10-209-208-2
; Sequence 2, Application US/10209208
; Sequence 2, Application US/10209208
; Publication No. US20050244921A1
; GENERAL INFORMATION:
   APPLICANT: Tsien, Roger
   APPLICANT: Tsien, Roger
   APPLICANT: Geoffrey Baird
   APPLICANT: Geoffrey Baird
; TITLE OF INVENTION: FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP2
; CURRENT APPLICATION NUMBER: US/10/209,208
; CURRENT APPLICATION NUMBER: US/10/209,208
; CURRENT APPLICATION NUMBER: 09/866,538
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR PILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR PILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR PILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 678
; NAME/KEY: misc feature
; LOCATION: (1):-.(678)
; OTHER INFORMATION: wild-type DsRed

US-10-209-208-2
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Alignment Scores:

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Sequence 2, Application US/11218880

Publication No. US20060003420A1

GENERAL INFORMATION:

APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC VARIANTS AND METHODS FOR MAI
TITLE OF INVENTION: WOMBER: US/11/218,880

FULR REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/10/121,258
PRIOR APPLICATION NUMBER: US/10/121,258

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2002-04-10

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26
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; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FASESEQ for Windows Version 4.
; SEQ ID NO 2
; LENGTH: 678
   TYPE: DNA
; ORGANISM: Discosoma sp.
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(678)
; OTHER INFORMATION: wild-type DsRed
US-11-218-880-2
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                                         HisHisLeuPheLeu
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                                                                                           IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
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APPLICANT: Teien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR APPLICATION NUMBER: 09/874,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 2001-02-26
PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE;
; OTHER INFORMATION: nucleotide sequence encoding DsRed with mammalian
; OTHER INFORMATION: codon usage
US-10-209-208-3
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Publication No. US20050244921A1
GENERAL INFORMATION:
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LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
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                                                                      MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
                                                                                                              AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACC
                                                 ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
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APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FOR MAKING SAME
TILLE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT PILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/966,538
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 681
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Publication No. US20050244921A1
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ORGANISM: Artificial Sequence
FEATURE:
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                AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                             LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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Sequence 3, Application US/11218880

Publication No. US20060003420A1

GENERAL INFORMATION:
APPLICANT: Taien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAK
FILE REFERENCE: UC083.1CP2CP1
CURRENT FLILING DATE: 2005-09-01
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/11/218,880
CURRENT FILING DATE: 2002-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 78

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 78
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                                                                                                                      US-10-006-922A-12 (1-225) x US-11-218-880-3 (1-681)
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US-11-218-880-3
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LENGTH: 681
TYPE: DNA
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21 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
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Gaps:
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                                                                                                                                                            FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/11/218,880
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
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Publication No. US20060003420A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC
TITLE OF INVENTION: PROTEIN VARIANTS AND
                                                                                        NUMBER OF SEQ ID NOS: 78
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 23
LENGTH: 681
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotide sequence encoding DsRed with mammalian
OTHER INFORMATION: codon usage
                                                                           TYPE: DNA
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Alignment Scores:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Sequence 4, Application US/10655872

Publication No. US20050251872A1

GENERAL INFORMATION:
APPLICANT: Bear, et al.
TITLE OF INVENTION: Lentiviral Vectors, Related RefFILE REFERENCE: 0492611-0512

CURRENT APPLICATION NUMBER: US/10/655,872

CURRENT FILING DATE: 2003-09-05

NUMBER OF SEQ ID NOS: 39

SOFTMARE: Patentin version 3.2

SEQ ID NO 4

LENGTH: 6706

TYPE: DNA

ORGANISM: Artificial
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; OTHER INFORMATION: lentiviral vector
US-10-655-872-4
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                                                                 Sequence 7, Application US/10655872 Publication No. US20050251872A1 GENERAL INFORMATION:
              APPLICANT: Bear, et al.
TITLE OF INVENTION: Lentiviral Vectors, ReFILE REFERENCE: 0492611-0512
CURRENT APPLICATION NUMBER: US/10/655,872
CURRENT FILING DATE: 2003-09-05
     NUMBER OF SEQ ID NOS:
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Matches:
Conservative:
Mismatches:
Indels:
Related Reagents,
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Percent Similarity:
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Query Match:
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RESULT 9
US-10-209-208-5
; Sequence 5, Application US/10209208
; Publication No. US20050244921A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
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US-10-655-872-7
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SEQ ID NO 7
LENGTH: 7927
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ORGANISM: Artificial
FEATURE:
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APPLICANT: GEOFFREY BAIRD
TITLE OF INVENTION: FLUORESCENT PROTEIN VARI
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UCO83.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DA
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                               IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                                                                    MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
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  TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC
                               TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
                                                                                                  ATCCACAAGGCCCTGAAGCTGAAGGACGGCCGCCACTACCTGGTGGAGTTCAAGTCCATC
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APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC VARIANTS AND METHODS FOR MAI
FILE REFERENCE: UCO83.1CP2CP1
CURRENT APPLICATION NUMBER: US/11/218,880
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US/9794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 678
LENGTH: 678
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Best Local Similarity:
Query Match:
DB:
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US-11-218-880-5
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleo
OTHER INFORMATION: "TI"
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                                                                                                                                                                                                                                                                                                                                                    MetArgSerSerLy8A8nVallleLy8GluPheMetArgPheLy8ValArgMetGluGly
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                                                                                                                                                                                                                         ACCCAGACCGCCAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATC 180
                                                                                                                                                                                                                                             H1sAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                                                             AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                                                                            CTGTCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGGCCGACATCCCC 240
                                                                                                                                                                            LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                 AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                            GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
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Matches:
Conservative:
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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR FILING DATE: 2001-02-26
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US-10-209-208-7
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
LENGTH: 681
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 80
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
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ThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSer
                                                                                                                  SerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGlyThrVal
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                                                     AACGGCCACGAGTTCGAGATCGAGGGCGAGGGCCAAGGGCCCCTACGAGGGCACCCAG 129
                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding DsRed polypeptide variant "dimer2"
                                                                                                                                                                                                                              2.15e-122
1121.00
95.96%
92.83%
92.34%
                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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Indels:
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Sequence 7, Application US/11218880

Publication No. US2006003420A1

GENERAL INFORMATION:

APPLICANT: Tsien, Roger

APPLICANT: Tsien, Roger

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAR

FILE REFERENCE: UC083.1CP2CP1

CURRENT FILING DATE: 2005-09-01

CURRENT FILING DATE: 2005-09-01

PRIOR APPLICATION NUMBER: US/11/218,880

CURRENT FILING DATE: 2002-04-10

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 78

SCETMARE: FastSEQ for Windows Version 4.0
                                                                                                                     ; OTHER INFORMATION:
; OTHER INFORMATION:
US-11-218-880-7
 Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                          LENGTH: 681
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CURRENT APPLICATION NUMBER: US/10/209,208
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/121,258
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                     Sequence 9, Application US/10209208
Publication No. US20050244921A1
GENERAL INFORMATION:
APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FUR MAKING SAME
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
RESULT 14
US-11-218-880-9
i Sequence 9, Application US/11218880
i Publication No. US20060003420A1
i GENERAL INFORMATION:
i APPLICANT: Tsien, Roger
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LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLI
TITLE OF INVENTION: PROTEIN VARIANTS AND ME
FILE REFERENCE: UCO83 1CP2CP1
CURRENT APPLICATION NUMBER: US/11/218,880
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/966,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOPTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 678
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ORGANISM: Artificial Sequence
FEATURE:
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TACATOGCCAAGAAGCCCCGTGCAGCTGCCCGGCGCCTACAAGACCGACATCAAGCTGGAC
             TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp 200
                                              ATCAAGATGAGGCTGAAGCTGAAGGACGGCGGCCACTACGACGCCGAGGTCAAGACCACC
                                                           IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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Sequence 80, Application US/10209208

Publication No. US20050244921A1

GENERAL INFORMATION:

APPLICANT: TSIEN, ROGER

APPLICANT: Campbell, Robert

APPLICANT: Geoffrey Baird

TITLE OF INVENTION: FOR MAKING SAME

FILE REFERENCE: UC083.1CF2CF2

CURRENT APPLICATION NUMBER: US/10/209,208

CURRENT FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: 10/121,258

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: 09/966,538

PRIOR APPLICATION NUMBER: 09/964,308

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 80

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 80

TVDE: DNA
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The present sequence is a novel fluorescent protein (nPP) encoded by the full-length cDNA drPP583. drPP583 was isolated from Discosoma sp. "red", a non-bioluminescent species of the Class Anthozoa. Pluorescent proteins can be used in fluorescent labeling, a useful tool for marking a protein, cell or organism of interest. Unlike other markers used in protein labeling, such as beta-galactosidase and luciferase, fluorescent proteins do not require an exogenous cofactor or substrate. Methods involving fluorescent proteins are also less laborious and less difficult to control than the traditional methods of fluorescent labeling, where a protein of interest is purified and then covalently conjugated to a fluorophore derivative. Novel fluorescent proteins isolated from species of the Class Anthozoa can be used as markers for gene expression and protein localization studies, and in fluorescence resonance energy
                                                                                                                                                                                                                                                                                                                   Novel fluorescent protein from non-bioluminescent useful for fluorescent labeling and as markers.
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Best Local
The present sequence is Discosoma sp. red fluorescent protein drFP583. It was isolated using the Aequoria victoria green fluorescent protein (GFP) sequence, which was used to design PCR primers which might isolate other fluorescent proteins from a number of species of Anthozoa. These were Anemonia majano, Clavularia sp., Zoanthus sp., Discosoma sp. and Anemonia sulcata. The cDNA obtained was then screened in the search for sequences encoding fluorescent proteins. The other proteins found in this manner were cFP484, zFP506, zFP538, amFP486, dsFP483, asFP600, dgFP512 and dmFP592. These proteins can be used as fluorescent labels (for gene expression and protein localisation studies and in fluorescence resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transfer (FRET) reactions. They may have improved properties and better suitability for larger excitations compared to prior art fluorescent proteins such as green fluorescent proteins such as green fluorescent protein. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anthozoa; fluorescent protein; fluorescence labeling; amFP486; cFP484; zFP506; zFP538; drFP583; dsFP483; asFP600; dgFP512; dmFP592.
                                                                                                                                                                              Claim 3; Page 68-69; 73pp;
                                                                                                                                                                                                          from non-bioluminescent
labeling and as markers.
                                                                                                                                                                                                                            Novel method for identifying a DNA sequence encoding fluorescent proteins from non-bioluminescent Anthozoa which are useful for fluorescent
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Best Local Similarity
Matches 225; Conserv
The invention provides a nucleic acid encoding functional red fluorescent CC protein (II) that differs from the sequence of an Anthozoan red fluorescent protein by at least one amino acid substitution, and with different fluorescent properties. The red fluorescent protein of the invention can be expressed by standard recombinant methodology. (II) are used a fluorescent markers and FRET partners. It is used for identifying protein-protein interactions. (II) is also suitable for multiplexed fluorescent analysis and FRET-based applications using existing Aequorea fluorescent proteins. (II) has improved brightness, reduced spectral cross talk, and is rapidly and efficiently expressed in mammalian cells. The key mutations in the encoding nucleic acids provide improved folding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               energy transfer (FRET) studies) in place of fluorophore derivatives and luciferases, as these involve laborious processes and the latter require cofactors. They can also be used in place of GFP, which is too stable to be useful when studying short-term or repetitive events
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Pred. No. 1e-127;
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The invention relates to DNA (I) containing either sequence ABA95905 or sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (yRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum or Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Escherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern biotechnology. (I) are optimised for expression in yeast and so generate RFP at higher levels with stronger fluorescence and thus lowers the detection limit and gives a better signal-to-noise ratio. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast; red fluorescent protein; RFP; plant; transgenic; GFP; Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis tha Escherichia coli; green fluorescent protein; biotechnology.
                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA encoding red fluorescent protein, biotechnology, has sequence optimized for
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The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications,
                                                                                                                                                                                                                                                                         New nucleic acid encoding a of an aggregating Chidarian analyte detection авваув or
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                                                                                                                                                                                                   Disclosure; Page 70-71; 80pp;
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N-PSDB;
The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer proteins are useful in monitoring the activity of a promoter, determining the age of a protein, identifying an agent that modulates the activity of a promoter and in enriching a population of cells comprising a fluorescent timer protein. The fluorescent timer proteins are also useful for assessing gene expression during development of a multicellular organism or during
                                                                                                                                                                                                                                                                                                            New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking
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Pred. No. 1e-127;
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cytotoxic compounds

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RESULT 7
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ID AAO18
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Best Local
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   Modified yeast strain, useful for detecting toxic compounds in environment, contains integrated cassettes responsive to genotoxic
                                                                                                                                                                                       Lichtenberg-Frate H;
                                                                                                                                                                                                                                                                                                              12-DEC-2000, 2000DE-01061872
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100.0%; Pred. No. 1e.
tive 0; Mismatches
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1e-127;
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Best Local Similarity
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New non-oligomerizing fluorescent protein containing at least one mutation that reduces or eliminates the ability of the protein to oligomerize, useful for making better and new assays for molecula:
                                                                                                                                                                                                                                                                                                                                                                          Discosoma sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADY51716 standard; protein; 225 AA
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                                                             WPI; 2002-713372/77.
N-PSDB; ADY51715.
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                                                                                                                                                                                                                                                                                                              Discosoma вр
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                                                                                                                                                                      26-FEB-2001; 2001US-00794308.
24-MAY-2001; 2001US-00866538.
                                                                                                                                                                                                                    26-FEB-2002; 2002WO-US006063
                                                                                                                                                                                                                                                                                                                                             fluorescence;
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                           mutagenesis; red
                                                                                                          Campbell
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Pred. No. 1e-127;
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Best Local
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 Novel chimeric phosphorylation indicators, useful for detecting
                                                                                                                                                24-MAY-2001; 2001US-00865291
                                                                                                                                                                                24-MAY-2002; 2002WO-US016955.
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                                                                                                                                                                                                                                                                             Discosoma sp.
                                                                                                                                                                                                                                                                                                             kinase;
                                                                                                                                                                                                                                                                                                                            Phosphorylation indicator; fluorescent protein; detection; phosphatase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE34962 standard; protein;
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                                 2003-148474/14.
DB; AAD53432.
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                                                                                Ting AY,
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100.0%; P:
ative 0;
                                                                                  Zhang
                                                                                                                                                                                                                                                                                                             protein;
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Pred. No. 1e-127;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or operative linkage, a donor molecule, a phosphorylatable domain, a phosphorylation binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Discosoma species red fluorescent protein (RFP) used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
                                                                                                                                                                                                                                                                                                                                                      Discosoma wild-type red fluorescent protein.
           N-PSDB; ADC24127, ADC24134.
                         WPI; 2003-743764/70
                                                                                                                                                                                                                                                       Discosoma
                                                                                                                                                                                                                                                                                 protein phosphatase;
                                                                                                                                                                                                                                                                                            fluorescent protein variant; transcription fluorescence energy resonance transfer; FRE
                                                                                                                                                                                                                                                                                                                           Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC24126 standard; protein;
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                                                      Tsien RY,
                                                                                  (TSIE/)
                                                                                                                          26-FEB-2001; 2001US-00794308
24-MAY-2001; 2001US-00866538
                                                                                                                                                                   10-APR-2002; 2002US-00121258
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                                                                                 TSIEN R Y.
CAMPBELL R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSPQPQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                                                     Campbell RE;
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Pred. No. 16
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a polynucleotide sequence (I) encoding a CC Discosoma red fluorescent protein (DBRed) variant having a reduced CC cand/or AC interfaces of the wild-type DBRed sequence (SI) comprising 225 amino acids, given in the specification, where the substitutions result (I) reduced propensity of the DBRed variant to form tetramers. (I) is CC useful for detecting transcriptional activity by providing a host cells CC conatining a vector which comprises (I) operatively linked to an CC expression control sequence, and an unit to assay the variant fluorescent protein fluorescence, and assaying fluorescence of the variant fluorescent cC fluorescence is indicative of transcriptional activity. A polynucleotide CC constination or trafficking of a polypeptide of interest. A polypeptide cC case is useful as markers to identify the location and amount of a CC target protein produced, where the target protein so the marker is seeful as markers to identify the location and amount of a CC target protein produced, where the target protein so the marker, CC which detects events as the function of the movement to the marker, applications involving fluorescence each other, for making CC interaction of a molecule such as Ca2+, Zn2+, for identifying the presence of a molecule such as Ca2+, Zn2+, for identifying the presence of a first and second molecule, for determining whether a CC useful for identifying a region or condition that regulates the activity of an expression control sequence. This is the amino acid sequence of Discosoma wild-type red fluorescent protein.
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Matches 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 225 AA;
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                                                                                                                                                                                                              ABW00918 standard;
                                    Fluorescent protein; resonance energy transfer; pH; detection; red fluorescent protein; RFP.
                                                                                             Discosoma sp. red fluorescent protein (RFP).
                                                                                                                                   15-JAN-2004
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                                                                                                                                   (first entry
                                                                                                                                                                                                              protein;
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RESULT 12
ADP70403
ID ADP70
XX ADP70
XX ADP70
XX ADP70
XX ADP70
XX L1-FE
XX L1-FE
XX Cell
XW Cell
XW GFPuv
XX GFPuv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
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                                                   ligand; orphan receptor protein; fusion protein; cell expression; green fluorescent protein; GFP; GFPuv; Enhanced GFP; EGFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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(ZACH/) ZACHARIAS D
(BAIR/) BAIRD G S.
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                                                                                                          Discosoma wild-type GFP variant protein SeqID26.
                                                                                                                                                                                            ADF70403 standard; protein; 225
                                                                                                                                       12-FEB-2004
                                                                                                                                                                  ADF70403;
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Pred. No. 1e-127;
; Mismatches 0;
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                                                                     fluorescent prote GFP-1; wild-type
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformation of cells with a fusion protein of an orphan receptor protein with a fluorescent protein useful for identification of ligands to the orphan receptor.
                                                                    Chromoprotein; fluorescent protein; CP; FP; intercon Chidnarian; Anthozoan; labelling; colouring agents; analyte detection assay; selectable marker; sunscree
                                                                                                                                  Discosoma
                                                                                                                                                             11-MAR-2004
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23-JUL-2002; 2002JP-00213949
11-OCT-2002; 2002JP-00298237
                           whole cell marker; second messenger detector; in fluorescence activated cell sorting; fluorescent
                                                           fluorescence resonance energy transfer; FRET; biosensor;
                                                                                                                                                                                          ADH34489;
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                                                                                                                                fluorescent protein DsRed (wild-type).
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CC different residues in the two types of proteins. Mutagenesis of the CC residues in these key positions in, for example, a fluorescent protein, CC to those found in a chromoprotein is therefore proposed to confer CC chromoprotein activity on the fluorescent protein mutant, with CC chromoproteins being able to be converted into fluorescent proteins in a CC similar manner. The invention also relates to expression constructs, CC vectors, host cells and host cell progeny comprising a nucleic acid of the invention; the recombinant production of an interconverted constructs, CC chromoprotein or fluorescent protein mutant; and antibodies specific for CC chromoprotein or fluorescent protein mutant; and antibodies specific for CC chromoprotein are useful in any application that employs a chromoprotein or fluorescent protein mutants having chromoprotein or clivity can useful as colouring agents in, for example, food CC compositions, pharmaceuticals, cosmetics and living organisms. Proteins CC with chromoprotein activity are also useful as labels in biological CC analyte detection assays, as selectable markers in recombinant DNA CC applications (e.g. the production of transgenic cells and organisms), and CC are also useful as sunscreens and selective filters. Chromoprotein CC ariants having fluorescent protein activity useful in fluorescence ce resonance energy transfer (FRET) applications, as biosensors in CC changes in multicellular reorganisation and migration, as second composition in biological membranes. Proteins with fluorescent protein composition in biological membranes. Proteins with fluorescent protein of proteins composition in biological membranes. Proteins with fluorescent protein of one of the protein composition in biological membranes. Proteins with fluorescent protein of one of the protein composition in biological membranes. Proteins with fluorescent protein composition in biological membranes. Proteins with fluorescent protein of one of the protein composition in biological membranes. Proteins with f
fluorescent colour to another (e.g., green to red) is concomitant with the ageing of the protein and is useful for determination of the activation or deactivation of gene expression. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GFP)-like chromoproteins and fluorescent proteins exhibit some degree homology, there are certain positions (referred to as 148, 165, 167 and 203; numbering corresponds to GFP) that are occupied by noticeably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to interconverted mutants of chromoproteins (CP)
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                                                                                                                    activity can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derived from a Cnidnarian
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protein activity. Corresponds
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protein activity. Corresponds to GFP residue 167"
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                                                                                                                membranes. Proteins with fluorescent protein as fluorescent timers, where the switch of or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     species, preferably a non-bioluminescent
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rresponds to GFP residue 148°
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Matches 225
                     The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods
                                                                                                                                                                                                                                                                                New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, usefi in molecular biology, e.g. in immunoassays or in tracking protein movement in cells.
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29-JUL-2002; 2002US-00209208.
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The present invention relates to nucleic acid that encodes a rapidly maturing chromo or fluorescent mutant of a Chidarian chromo- or fluorescent protein or its mutant. The protein is useful in applications involving nucleic acid encoding a chromo- or fluorescent protein and is useful for producing a chromo and/or fluorescent protein which involves growing the cell, whereby the protein is expressed, and isolating the protein substantially free of other proteins. The protein is useful in applications involving chromo- or fluorescent protein and is useful as pocked the protein and is useful as protein substantially free of other proteins. The protein and is useful as applications involving chromo- or fluorescent protein and is useful as pocked protein and is useful as protein and is usefu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC useful for synthesizing related proteins. The chromoproteins are useful CC as coloring agents which are capable of imparting color or pigment to a CC particular composition of matter e.g., food compositions, pharmaceuticals, CC cosmetics, living organisms, e.g., animals and plants. The chromoproteins CC may also find use as labels in analyte detection assays, e.g. assays for Diological analytes of interest and as selectable markers in recombinant CC DNA applications, e.g. the production of transgenic cells and organisms. CC e.g. in fluorescence resonance energy transfer (FRET) applications, as colorence of the automated screening of arrays of cells expressing fluorescent crapbrications involving the automated screening of arrays of cells expressing fluorescent crapbrications by using microscopic imaging and electronic analysis, as cond messenger detectors, and in fluorescence activated cell sorting applications and as in vivo marker in animals. The fluorescent proteins calso find use in protease cleavage assays. The sproteins can also be used is assays to determine the phospholipid composition in biological common and as a fluorescent timer. The present sequence represents the wild-type DsRED.
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Best Local S
Matches 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma sp. red fluorescent protein (RED).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2004
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ilarity 100.0%;
Conservative 0
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                                                                              note= "Loop region'
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ce= "Loop region"
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Pred. No. 1e-127;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fluorescent protein;
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RESULT 17
ADM97769
ID ADM977
XX ADM97
XX ADM97
XX O1-JU
DT 01-JU
DT 0 sp
XX Enzym
KW enzym
KW enzym
KW targe
XX Signa
KW targe
XX Discc
XX Discc
XX WO200
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Best Local S
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                                                               enzyme; sensor cell; signal transduction c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to binding ligands (fluorobodies) with intrinsic fluorescence, which comprises green fluorescent protein (GFP) having heterologous binding sites. The binding ligand is useful for detecting the target molecule and is efficiently detects the target molecule. The present sequence is Discosoma sp. red fluorescent protein (RBD) used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel binding ligand with intrinsic fluorescence and comprising fluorescent protein having heterologous binding sites, useful for detecting target molecule.
                                                    targeted
                                                                                                                                      01-JUL-2004
                                                                                                                                                                                         ADM97769 standard; protein; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 225 AA;
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                                                                                                         sp red fluorescent protein SEQ ID
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DB; ADI36420.
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                                                                                                                                                                                                                                                                                                                                      KVKFIGVNFPSDGPVMQKKTMGWEASTERLYFRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                      LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                                                                                                                                                                                                                                                                                      YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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                                                                                                                                      (first entry)
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                                                               green fluorescent protein; detection system; promoter; targeting sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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Pred. No. 1e-127;
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WO2004031415-A2 Discosoma sp.

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RESULT 18
ADQ28780
ID ADQ28
XX
AC ADQ28
XX
O7-OC
XX
Jelly
XX
XW
Green
XX
KW
Green
XX
KW
Green
XX
WO20C
XX
MO20C
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PD 15-Ju
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Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method of developing a sensor cell, for determining the activity of a target gene in the cell, which comprises providing a homogeneous population of cells, where each of the cells comprises a signal transduction detection system and introducing into the population of cells an isolated DNA construct comprising a promoter operatively linked to a targeting sequence. The method is useful in developing a sensor cell for determining the activity of a target gene in the cell. The sensor cell and the methods are useful in developing new and therapeutic drugs directed to the targets. The present sequence is a polypeptide shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developing a sensor cell, useful in determining the activity of a targene and in developing therapeutic drugs, comprises providing cells comprising a signal transduction detection system and introducing DNA construct into cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 225 AA;
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                                                                                                                             Jellyfish green fluorescent protein
                                                                                                                                                           07-OCT-2004
                                                                                                                                                                                                                   ADQ28780 standard; protein;
                                             WO2004058973-A1
                                                                      Aequorea victoria
                                                                                                                                                                                        ADQ28780;
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                                                                                                   fluorescent protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLFFAWDI
                                                                                                                                                                                                                                                                                                             YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                           LSPQPQYGSKVYVKHPADIPDYKKLSPPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                          YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                           (first entry)
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                                                                                                     fluorescent protein
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Pred. No. 1e-127;
; Mismatches 0;
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                                                                                                                                 DaRed
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RESULT 19
ADX26534
ID ADX26
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문
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Best Local Similarity
Matches 225; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel coding sequences (I) encoding green fluorescent proteins (II). The fluorescent protein coding sequences are isolated from an organism from phylum Arthropoda, from subclass Copepoda, or from family Pontellidae. The fluorescent protein coding sequences are useful for labelling biomolecules, cell, or cell organelles. They are also useful for identifying expression of a gene in a biological specimen or for generating transformants including transgenic organisms or site-specific gene modifications in cell lines. The present sequence was useful in high throughput screening assays. The present sequence was used in a sequence alignment with the green fluorescent proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule encoding a fluorescent protein, usefi for labeling biomolecules, cell, or cell organelles, or for identifying expression of a gene in a biological specimen.
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02-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EVRO=) EVROGEN STOCK
                                                                                                                                                           Discosoma DsRed
                          28-MAY-2004;
                                                    03-FEB-2005
                                                                                                                                 Phosphorylation;
                                                                                                                                                                                     21-APR-2005
                                                                                                                                                                                                              ADX26534;
                                                                                                                                                                                                                                         ADX26534 standard;
                                                                             US2005026234-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTVQDSSLQDGCFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AA;
                                                                                                                                                                                                                                                                                                          YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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2003US-0459679P
                          2004US-00857622
                                                                                                                                                                                     (first
                                                                                                                                                          RFP protein,
                                                                                                                                  detection;
                                                                                                                                                                                                                                         protein;
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                                                                                                                                                          seq id 12.
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Pred. No. 1e-127;
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                                                                                                                                     fluorescent
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31-JAN-1996;

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Best Local :
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13-SEP-1999;
24-MAY-2001;
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 protease; assay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric phosphorylation indicator comprises a first fluorescent protein, phosphoaminoacid binding domain with FHA2 sequence and proteinage C-phosphorylatable domain, useful for detecting protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
 Autofluorescent; fusion protein; proteolytic activity; protease; assay; protease cleavage.
                                                 Autofluorescent fusion protein A SEQ ID NO 1.
                                                                                 28-MAY-2002
                                                                                                                  ABB08821
                                                                                                                                                 ABB08821 standard; protein; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 225
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cal Similarity 100.0%;
225; Conservative 0
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) NEWTON A C.
) TSIEN R Y.
) ZHANG J.
                                                                                                                                                                                                                                                  YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60
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99US-00396003.
2001US-00865291.
                                                                                (first
                                                                                 entry)
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Pred. No. 1e-127;
; Mismatches 0;
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                 fluorophore;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New autofluorescent fusion protein, useful for determining protease and protease-inhibiting activity, comprises two different proteins linked by
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                             protease;
                                           Autofluorescent;
                                                                        Autofluorescent fusion protein B SEQ ID NO
                                                                                                       28-MAY-2002
                                                                                                                                    ABB08822
                                                                                                                                                                ABB08822 standard; protein; 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DIRE-) DIREVO BIOTECH AG.
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                                                                                                                                                                                                                                                             YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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                              аввау;
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                                                                                                       (first entry)
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                             fusion protein; proteolytic activity; protease cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Pred. No. 3.2e-127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 506 AA;
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                                                                                                            Autofluorescent; protease; assay;
                                                                                                                                                                                                                                                     28-MAY-2002
                                                                                                                                                                                                                                                                                                             ABB08823
     WO200212543-A2
                                                                                                                                                                                           Autofluorescent fusion protein C SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                              ABB08823 standard;
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                                                                                                            fusion protein; proteolytic activity;
protease cleavage.
                                                                                                                                                                                                                                                                                                                                                              protein;
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Pred. No. 3.4e-127;
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                                                                                                                                               fluorophore;
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RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New autofluorescent fusion protein, useful for determining protease and protease-inhibiting activity, comprises two different proteins linked by
                                            Pluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay sunscreen; second messenger detector; drPP583 protein; NFP-6; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                     Discosoma
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ilarity 100.0%;
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                                                                                                                                     drFP583 (NFP-6) mutant protein,
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Pred. No. 3.8e-127;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drFP583 (NFP-6) wild-type protein shown as SEQ ID NO:8 (AAR28833) in page 70-71 of the specification
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of an aggregating Chidarian chromo- or fluorescent panalyte detection assays or fluorescence activated of
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04-DEC-2001;
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 Discosoma вр.
                             15-JAN-2004
                                                         ABW00937;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 225
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2001US-00006922.
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                             (first entry)
 red fluorescent protein (RFP), S197T.
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                                                                                    protein;
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Pred. No. 2.2e-127;
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    or fluorescent mutant
protein or mutant for
cell sorting

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RESULT 25 ABW00929

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standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fluorescent proteins containing a mutation that reduces or eliminates i ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsien RY, Zacharias
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Synthetic.
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) ZACHARIAS D A.
) BAIRD G S.
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                                                                                                                                                                                                                                                                                                MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                           LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                       YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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  YMAKKPVQLPGYYYVDTKLDITSHNEDYTIVEQYERTEGRHHLFL
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protein; RFP; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                            Score 1211; DB 7;
Pred. No. 2.2e-127;
1; Mismatches 0;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fluorescent proteins containing a mutation that reduces or eliminates is ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
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                                                                                                                                                                                                                                                             Sequence 225 AA;
                                                                                                                                                                                                                                                                                    sequence is constructed based on Discosoma sp.
shown in page 30-31 (ABW00918)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prescent protein; resonance energy fluorescent protein; RFP; mutant;
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ZACHARIAS D A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baird
                                                                                                                                                                                                           1;
                                                                                                                                                                                                                        Score 1211; DB 7;
Pred. No. 2.2e-127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
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Synthetic.
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                                                                                                                                                                                                                                                  Sequence 225
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YMAKKPVQLPGYYYVDSKLDITSHNBDYTIVBQYERTBGRHHLFL
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                                                                                         LSPQFQYGSRVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSPPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                             MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                            99.8%;
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                                                                                                                                                                                                            Score 1211; DB 7;
Pred. No. 2.2e-127;
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181 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225

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RESULT 27
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                   The invention relates to interconverted mutants of chromoproteins (CP) or CC fluorescent proteins (FP) and nucleic acids encoding them. The mutant is CC derived from a Chidnarian species, preferably a non-bioluminescent CC chidarian species, and most preferably an Anthozoan species. The CC invention is based on the finding that although green fluorescent protein CC (GFP)-like chromoproteins and fluorescent proteins exhibit some degree of homology, there are certain positions (referred to as 148, 165, 167 and CC 203, numbering corresponds to GFP) that are occupied by noticeably CC different residues in the two types of proteins. Mutagenesis of the CC residues in these key positions in, for example, a fluorescent protein, CC chromoprotein activity on the fluorescent protein mutant, with recombinations being able to be converted into fluorescent proteins in a similar manner. The invention also relates to expression constructs, cc to those cells and host cell progeny comprising a nucleic acid of CC enromoprotein or fluorescent protein mutant; and antibodies specific for CC invention; the recombinant production of an interconverted CC interconverted mutant protein mutant; and antibodies specific for CC interconverted mutant protein sof the invention. The interconverted context are useful in any application that employs a chromoprotein or fluorescent protein mutants having chromoprotein cCC compositions, pharmaceuticals, cosmetics and living organisms. Proteins with chromoprotein activity are also useful as labels in biological canalyte detection activity are also useful as labels in biological and organisms. Proteins and protein cells and organisms. and and protein cells and organisms. And and protein cells and organisms. And and analyte detection activity are also useful as labels in any arganisms. And any the detection activity are also useful as labels in all arganisms. And any the detection activity are also activity and activity and any the detection activity are also activity and activity and activity are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding interconverted mutant of chromo-or fluorescent protein which are useful as biosensors, coloring ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CLON-) CLONTECH LAB INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutant
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   in recombinant DNA cells and organisms), and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC are also useful as sunscreens and selective filters. Chromoprotein CC mutants having fluorecent protein activity useful in fluorescence cresonance energy transfer (FRET) applications, as biosensors in CC prokaryotic and eukaryotic cells, as markers of whole cells to detect CC changes in multicellular reorganisation and migration, as second comessenger detectors, as in vivo markers in animals (e.g., transgenic clanges), in fluorescence activated cell sorting applications, in CC protease cleavage assays, and in assays to determine the phospholipid CC composition in biological membranes. Proteins with fluorescent protein CC fluorescent colour to another (e.g., green to real) is concomitant with CC the ageing of the protein and is useful for determination of the CC activation or deactivation of gene expression. The present sequence CC represents a Discosoma sp. red fluorescent protein DaRed mutant generated CC in an example of the invention. The present sequence is not shown in the specification, but was derived from the wild-type DaRed sequence (ADH34489) shown in Fig 1 and the information provided on page 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                        Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidmarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable marker; sunscreen; selective f fluorescence resonance energy transfer; FRET; biosensor;
              23-DEC-2002; 2002WO-US041418
                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                        whole cell marker; second messenger detector; in vivo marker; fluorescence activated cell sorting; fluorescent timer;
                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004
                                                17-JUL-2003.
                                                                                 WO2003057833-A2
                                                                                                                                                      Misc-difference
                                                                                                                                                                                                       Discosoma
                                                                                                                                                                                                                                                       red fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                 Discosoma sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH34499 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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hes 224;
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24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRSSKNVIKEFMRFKVRMEGTVNGHEFBIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVKFIGVNFPSDGPVMQKKTMGWEAATERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                       gp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 DsRed mutant
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                           protein;
                                                                                                                   residue
                                                                                                                                    /note= "Ala replaces wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%;
                                                                                                                                                                                                                                                           DsRed; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                   S203A.
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Pred. No. 2.2e-127
1; Mismatches 0
                                                                                                                                                                                                                                                           mutein.
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                                                                                                                                     Corresponds
                                                                                                                                                                                                                                                                                                                              selective filter;
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26-DEC-2001; 2001US-0343128P

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cc fluorescent proteins (FP) and nucleic acids encoding them. The mutant is converted mutants of chromoproteins (CP) or derived from a Chidarian species, preferably a non-bioluminescent condition is based on the finding that although green fillourescent protein (GPP)-like chromoproteins and fluorescent proteins explain some degree of homology, there are certain positions (referred to as 148, 165, 167 and CO 303) numbering corresponds to GPP) that are occupied by noticeably conditions in the two types of proteins exhibit some degree of the condition in the conditions in, for example, a fluorescent protein creations in a chromoprotein is therefore proposed to confer chromoprotein being able to be converted into fluorescent proteins in a circumpercein being able to be converted into fluorescent protein mutant, with converted manner. The invention also relates to expression constructs, call any other call progeny comprising a nucleic acid of the invention; the recombinant protein mutant; and antibodies specific for interconverted mutant protein activity are also useful as intromoprotein or fluorescent protein mutant; and antibodies specific for interconverted mutant protein activity are also useful as labels in biological analyte detection activity are also useful as labels in biological analyte detection, as in vivo markers in animals (e.g., the production of transpends cells and organisms), and carease clawage assays, as selectable markers of whole cells to detect changes in multicellular reorganisation and migration, as second compositions in also be used as fluorescent there, where the switch of one sensors and subcrition in biological membranes. Proteins with fluorescence composition in biological membranes. Proteins with fluorescence composition in biological membranes. Proteins with fluorescence of composition in biological membranes. Proteins with fluorescent protein cativity can also be used as fluorescent there, where the switch of one fluorescent protein and is useful for determination of the composition
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                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                             Matches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid encoding interconverted mutant of chromo-or fluorescent protein which are useful as biosensors, coloring agents.
                                                                                                                                                                                                                                                                                                          Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLON-) CLONTECH LAB INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Page; 56pp; English.
                                                                                                  LSPQPQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDI
                                                                                                                                                     MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLFFAMDI
                      KVKFIGVNFPSDGFVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                          LSPQFQYGSKVYVKHPADIPDYKKLSPPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                  99.8%;
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                                                                                                                                                                                                                                                    Score 1211; DB 7;
Pred. No. 2.2e-127;
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                      Length 225;
                                                                                                                                                                                                                                    Indels
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MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVIKGGPLFFAWDI

Query Match Best Local

Similarity

99.78;

Score 1210; Pred. No. 2

Length Indels

υΒ 5; -... No. 2.9e-127; Mismatches

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Gaps

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XX M Siscc
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                                                       The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in protein and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. darPp583 (NPP-6) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. darPp583 (NPP-6) wild-type protein shown as SEQ ID NO:8 (AAE28833) in page 70-71 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Cnidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; NFP-6; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Discosoma sp. Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page; 80pp; English
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04-DEC-2001;
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      Sequence
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      225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0270983P
2001US-00006922
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Query Match
Best Local Similarity
                                                                                                                                    The invention relates to a non-oligomerising fluorescent protein containing a mutation that reduces or eliminates its ability to oligomerise. The fluorescent protein gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH. These are also used to identify agents or conditions that regulate expression of control sequences. The present sequence is Discosoma sp. red fluorescent protein (RFP) mutant. Note: This sequence is not shown in the specification, however this sequence is constructed based on Discosoma sp. wild-type RFP protein shown in page 30-31 (ABW00918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                               Sequence 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-802418/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZACHARIAS D A.
BAIRD G S.
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cent protein; RFP; mutant;
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99.6%;
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  Score 1210; DB 7; Pred. No. 2.9e-127;
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                           The invention provides a nucleic acid encoding functional red fluorescent CC CC protein (II) that differs from the sequence of an Anthozoan red CC fluorescent protein by at least one amino acid substitution, and with CC different fluorescent properties. The red fluorescent protein of the CC invention can be expressed by standard recombinant methodology. (II) are CC used a fluorescent markers and FRET partners. It is used for identifying CC protein-protein interactions. (II) is also suitable for multiplexed CC fluorescent analysis and FRET-based applications using existing Aequorea CC fluorescent proteins. (II) has improved brightness, reduced spectral CC cross talk, and is rapidly and efficiently expressed in mammalian cells. CC The key mutations in the encoding nucleic acids provide improved folding, CC brightness, and create (II) with sharper, more defined excitation and CC brission peaks when expressed in mammalian cells. The present sequence CC represents the amino acid sequence of an improved synthetic mutant of an CC anthozoan fluorescent protein
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Query Match

Score 1210;

DB 4;

Length 226;

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This invention describes a novel method of site-specific DNA recombination in eukaryotic cells in vitro comprising using a bacteriophage Pl Cre recombinase that lacks heterologous protein-created comming the recombinase that lacks heterologous protein-created comming site-specific DNA recombination also contains a reporter system for detecting site-specific DNA recombination in eukaryotic cells.

CR Recombination with Cre recombinase lacking heterologous protein-created cells, in vivo or in vitro, e.g. for partial inactivation creates a chromosomal translocation. The created cells in vivo or in vitro, e.g. for partial inactivation creates a chromosomal translocation. The created cells when added to culture medium and catalyzes recombination created cells when added to culture medium and catalyzes recombination created cells when added to culture medium and catalyzes recombination created cells introduced into the cell, so its effect is immediate but short-lived, limiting cytotoxic effects; eliminating the risk of non-creatific integration of DNA into the genome and providing quick results.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; SEQ ID NO 6; 84pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inactivation, using transduction domain
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16-JUL-2002; 2002DE-01032196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reporter
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1; Mismatches 0;
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RESULT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 224;
The present invention describes a chimeric protein comprising at least one signal protein that has a trafficking signal targeting to a subcellular organelle and at least one proteolytic cleavage site for a protease. The chimeric protein is constructed, so that: (a) the trafficking signals of all the signal proteins are inactivated by linking the proteolytic site or a signal masking protein through the proteolytic site or a signal masking protein through the proteolytic site to the N-or C- terminus of the signal proteins, and so the chimeric protein is present in cytosol; (b) the trafficking signal of at least one signal protein is activated when the proteolytic cleavage site is cleaved by the protease, and as a result at least one fragment protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric protein; proteolytic cleave
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                                                                                                                                                                                                                                                      Hwang
                                                                                                                                                                                                                                                                                                                                    08-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL18132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL18132 standard; protein; 545 AA.
                                                                                                                                                                        New chimeric protein, useful for detecting protease inhibitors inside the cell or tissue.
                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                         10-AUG-2001; 2001KR-00048123
                                                                                                                                                                                                                                                                                                                                                                20-FEB-2003
                                                                                                                                               Example 2; SEQ ID NO 52; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              Tobacco vein mottling virus
                                                                                                                                                                                                                                                                                (AHRA-)
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                                                                                                                                                                                                                 ADL18131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YMAKKPVOLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                        Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease):AtOEP7:GFP fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal protein; trafficking
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal targeting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana. Human immunodeficiency
   N-PSDB; ADL18155
                                       WPI; 2003-256596/25
                                                                                              Hwang I,
                                                                                                                                                                                                                   10-AUG-2001; 2001KR-00048123.
                                                                                                                                                                                                                                                                                 08-AUG-2002; 2002WO-KR001515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFP:PS(HIV-1 protease):AtOEP7:GFP fusion protein SEQ ID NO:76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVKFIGVNFPSDGFVMQKXTMGWBASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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                                                                                                 Kim DH,
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                                                                                                                                                               BIOSYSTEMS INC.
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age site; protease; protease inhibitor
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Pred. No. 1.1e-126;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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New chimeric protein, useful for detecting cell or tissue. protease inhibitors inside the

Example 3; SEQ ID ğ 76; 214pp; English.

The present invention describes a chimeric protein comprising at least come signal protein that has a trafficking signal targeting to a composition of signal protein that has a trafficking signal targeting to a composition of the protease. The chimeric protein is constructed, so that: (a) the content of the proteolytic site or a signal masking protein are inactivated by linking the proteinlytic constructed, so that: (a) the content to the Norce terminus of the signal proteins are inactivated by linking the proteinlytic constructed, so the chimeric content in the protein is activated when the proteins, and so the chimeric protein is protein is activated when the proteins, and so the chimeric concludes the activated when the protein that constructed to a subcellular conganalle; and (c) the chimeric protein is a transported to a subcellular conganalle; and (c) the chimeric protein is a transported to a subcellular conganalle; and the position and intensity distribution of the cleavage by the protease. Also described: (1) a recombinant gene comprising a concluded acid sequence encoding the chimeric protein which is constructed to express the chimeric protein in a cell; (2) a cell transformed with the recombinant gene or vector; (3) analysing the activity of a protease invivo; (4) sorrening protease inhibitors in vivo; (5) a system for congrising the chimeric protein or the vector; (c) a cell; (7) a vector comprising the nucleic acid; (8) a kit for detecting a protease inside a cell comprising the chimeric protein or the vector; (c) detecting a protease inside a cell or tissue, and (10) detecting a constant invention protein, which is used in the exemplification of the crease inhibitors in vivo; The chimeric protein is useful for detecting constant a fusion protein, which is used in the exemplification of the crease inhibitors inside the cell or tissue. The present sequence present invention.

Sequence 548 AA;

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182
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                  YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                       KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                          LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                             MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                     KVKF1GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE1HKALKLKDGGHYLVEFKS1
                                                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                              VRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                               99.7%;
                                                                                                                                                                                                                Score 1210; DB 7;
Pred. No. 1.1e-126;
1; Mismatches 0;
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AAE28922 standard; protein; 225 B

Discosoma sp. drFP583 (NFP-6) mutant protein, 四8 (N42H).

27-DEC-2002

(first entry)

Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; NFP-6; mutant;

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RESULT 36
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Best Local &
Matches 224
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in protein and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drrp583 (NFP-6) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drrp583 (NFP-6) wild-type protein shown as SEQ ID NO:8 (AAE28833) in page 70-71 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Discosoma
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding a non-aggregating chromo- or fluorescent moof an aggregating Chidarian chromo- or fluorescent protein or mutant analyte detection assays or fluorescence activated cell sorting
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04-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page; 80pp;
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                ABW00936;
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                                           ABW00936 standard;
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                                                                                                                                                                                      KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                         LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
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                                                                                                                                  YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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2001US-00006922.
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                                          protein; 225 AA
                                                                                                                                                                                                                                                                                                                                                     99.6%;
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                                                                                                                                                                                                                                                                                                                                        Score 1209; D)
Pred. No. 3.8e
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.8e-127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzymes, or sample pH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TSIE/)
(ZACH/)
(BAIR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001;
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Synthetic.
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                                                                                                                                                                                                                                                                      Sequence 225
                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZACHARIAS
                                                                                                                                                                           WRSSKNVIKEFMRFKVRMEGTVNGHEFBIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                             MRSSKNVIKEFWRFKVRMEGTVNGHEFEIEGEGEGRFYEGHNTVKLKVTKGGPLFFAMDI
              YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                  KVKFIGVNFPSDGPVMOKKTMGWEASTERLYPRDGVLKGEI1KALKLKDGGHYLVEFKSI 180
                                                                                                       LSPQFQYGSKVYVKHPADIPDYKKLSPPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIH
                                                                                                                        LSPQFQYGSKYYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                    KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baird
                                                                                                                                                                                                                   Score 1209; DB 7;
Pred. No. 3.8e-127;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is substituted with His"
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                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                               mutant.
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RESULT 37 ABW00931

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fluorescent proteins containing a mutation that reduces or eliminates is ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzymes,
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 181
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BAIRD G S.
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                                                                                                                                                                                                                 Similarity
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                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                       225
                                                                                                                                                                                                                                                                                                                                                                                                                                                or sample pH
              YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                 KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                               KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                   LSPQFQYGSKVYVKHPADIPDYNKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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ein; RFP; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baird
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                                                                                                                                                                                                    Score 1209; DB 7;
Pred. No. 3.8e-127;
0; Mismatches 1;
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RESULT 38
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                        The invention relates to DNA (I) containing either sequence ABA95905 or sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (YRFP). (I) are used to express red fluorescent protein (RFP) in enkaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum or Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Escherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern biotechnology. (I) are optimised for expression in yeast and so generate RFP at higher levels with stronger fluorescence and thus lowers the detection limit and gives a better signal-to-noise ratio. The present sequence is that of the yeast optimised RFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       especially yeast or plants.
                                                                                                                                                                                                                                                                                                 Sequence 226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 15; 19pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE20001395-U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast optimised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding red fluorescent protein, useful as marker biotechnology, has sequence optimized for expression in euk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GPCB-) GPC BIOTECH AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-228394/29.
183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        red fluorescent protein; RFP; plant; transgenic; GFP; romyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana; ichia coli; green fluorescent protein; biotechnology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA95906
               MAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                            VKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIY 181
                                                                                                                    SPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYK 122
                                                                                                                                     SPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYK 121
                                                                                                                                                                              RSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDIL 62
                                                                                                                                                                                             RSSKNVIKBFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDIL
                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                      Score 1209; DB 5; ]
Pred. No. 3.8e-127;
0; Mismatches 0;
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RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a non-oligomerising fluorescent protein containing a mutation that reduces or eliminates its ability to oligomerise. The fluorescent protein gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH. These are also used to identify agents or conditions that regulate expression of control sequences. The present sequence is Discosoma sp. red fluorescent protein (RFP) mutant. Note: This sequence is not shown in the specification, however this sequence is constructed based on Discosoma sp. wild-type RFP protein shown in page 30-31 (ABW00918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-802418/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzymes, or sample pH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001US-00794308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001US-00794308.
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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) ZACHARIAS D A.
) BAIRD G S.
                                                                                                                                                                                                   LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                             MRSSKAVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDI
                                                                                                                                                                   LSPQFQYGSKVYVKHPADIPDYPKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
  YMAKKPYQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                      KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fluorescent
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Pred. No. 4.9e-127;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                               Fluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fluorescent protein; resonance energy transfer; pH; red fluorescent protein; RFP; mutant; mutein.
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                                                                                                                                                                                          Sequence 225 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsien RY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TSIE/) TSIEN R Y.
(ZACH/) ZACHARIAS
(BAIR/) BAIRD G S.
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                                                                                                                                                   Local Similarity
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121
                                                                                                                                     224;
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                                                                                                                                                                                                                                                                                                                                                                                                     or sample pH
                                            LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMVFEDGGVVTVTQDSSLQDGCFIY
KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                           LSPQFQYGSKVYVKHPADIPDYMKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                      Conservative
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                                                                                                                                                  99.5%;
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Pred. No. 4.9e
O; Mismatches
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                                                                                                                                                  4.9e-127;
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                                                                                                                                                                Length 225;
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                                                                       Matches
                                                                                                                                        containing a mutation that reduces or eliminates its ability to oligomerise. The fluorescent protein gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH. These are also used to identify agents or conditions that regulate expression of control sequences. The present sequence is Discosoma sp. red fluorescent protein (RFP) mutant. Note: This sequence is not shown in the specification, however this sequence is constructed based on Discosoma sp. wild-type RFP protein shown in page 30-31 (ABW00918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma
Synthetic.
                                                                                                                                                                                                                                                                                                                Fluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                                                                       Sequence 225 AA;
                                                                                                                                                                                                                                                      The invention relates to a non-oligomerising fluorescent protein
                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                       enzymes,
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-802418/75
                                                                                                                                                                                                                                                                                                                                                                                         Tsien RY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001US-00794308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fluorescent protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Discosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (TSIE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                 (BAIR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fluorescent
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 61
                                                                                                                                                                                                                                                                                                                                                                                                                 ZACHARIAS DA.
BAIRDGS.
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         TSIEN R Y.
                                                                                                                                                                                                                                                                               2; Page; Opp; English.
 LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                        MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                       or sample pH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                       MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fluorescent
                                                                                  99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resonance energy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFP;
                                                                                                                                                                                                                                                                                                                                                                                          Baird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225
                                                                      Score 1208; DB 7;
Pred. No. 4.9e-127;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is substituted with Met"
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RESULT 42
ADH3490
ADH341
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AC ADH34
AC ADH34
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AC ADH34
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fluorescent proteins (FP) and nucleic acids encoding them. The mutant is derived from a chidnarian species, preferably a non-bioluminescent chidarian species, and most preferably an Anthozoan species. The invention is based on the finding that although green fluorescent protein (GFP)-like chromoproteins and fluorescent proteins exhibit some degree of homology, there are certain positions (referred to as 148, 165, 167 and 203; numbering corresponds to GFP) that are occupied by noticeably different residues in the two types of proteins. Mutagenesis of the residues in these key positions in, for example, a fluorescent protein, to those found in a chromoprotein is therefore proposed to confer chromoprotein activity on the fluorescent protein mutant, with chromoproteins being able to be converted into fluorescent proteins in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidnarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable marker; sunscreen; selective filter;
                                                                                                                                                                                                                                                                                                                                                                           The invention relates to interconverted mutants of chromoproteins (CP)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding interconverted mutant of chromo-or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2001; 2001US-0343128P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fluorescence resonance energy transfer; FRET; biosensor;
whole cell marker; second messenger detector; in vivo marker;
fluorescence activated cell sorting; fluorescent timer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Discosoma вр.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-2002; 2002WO-US041418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003057833-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CLON-) CLONTECH LAB INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGBIHKALKLKDGGHYLVBFKSI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chudakov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; DsRed; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Ala replaces wild-type residue 148"
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residue 203"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lukyanov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosensors, coloring agents.
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ARESULT 43
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KW Fluor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc vectors, host cells and host cell progeny comprising a nucleic acid of che invention; the recombinant production of an interconverted content or fluorescent protein mutant; and antibodies specific for interconverted mutant proteins of the invention. The interconverted content protein mutant; and antibodies specific for content or the protein mutant; and antibodies specific for content or useful in any application that employs a chromoprotein or content protein mutants having chromoprotein compositions, pharmaceuticals, cosmetics and living organisms. Proteins compositions, pharmaceuticals, cosmetics and living organisms. Proteins compositions (e.g. the production of transgenic cells and organisms) and compositions (e.g. the production of transgenic cells and organisms), and care also useful as subscreens and selective filters. Chromoprotein composition as subscreens and selective filters. Chromoprotein composition and eukaryotic cells, as markers of whole cells to detect changes in multicellular reorganisation and migration, as second composition in biological membranes. Proteins with fluorescent protein composition in biological membranes. Proteins with fluorescent protein composition in biological membranes. Proteins with fluorescent protein composition or deactivation of suseful for determination of the activity can also be used as fluorescent timers, where the switch of one cativity can also be used as fluorescent timers, where the switch of one cativity can also be used as fluorescent timers, where the switch of one cativity can also be used as fluorescent timers, where the switch of one cativity can also be used as fluorescent timers, where the switch of one cativity can also be used as fluorescent protein barded mutant generated in an example of the invention. The present sequence is not shown in the specification, but was derived from the wild-type DaRed mutant genera
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                                                                                                                                                                                                                                                                                               27-DEC-2002
                                                                                                                                                                                                                                                                                                                                           AAE28921;
                                                                                                                                     Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; blosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay;
                                                                                                                                                                                                                                                                                                                                                                                     AAE28921 standard;
                       Discosoma sp
Synthetic.
                                                                                                             sunscreen; second messenger detector; drFP583
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                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                  drFP583 (NFP-6) mutant
                                                                                                                                                                                                                                                                                                                                                                                     protein; 225
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Pred. No. 4.9e-127;
2; Mismatches 0;
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                                                                                                                                                                                                                                                  protein,
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RESULT 44
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Best Local S
Matches 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drFP583 (NFP-6) wild-type protein shown as SEQ ID NO:8 (AAE28833) in page 70-71 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type Val substituted with Ala" Misc-difference 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a non-aggregating chromo-
of an aggregating Chidarian chromo- or fluorescent p
analyte detection assays or fluorescence activated c
applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-691654/74.
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04-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                      MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLFFAMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AA;
                                                                                      standard;
                                                                                                                                                                           YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                      KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                       KVKFIGVNFPSDGPVMQKKTWGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                            YMAKKPVOLPGYYYVDTKLDITSHNEDYTIVEOYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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2001US-00006922
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                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                            99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yanushevich Y,
                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 1207; DB 5;
Pred. No. 6.3e-127;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Savistky A,
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nt for
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**Discosoma** вр. 22-APR-2002

fluorescent protein

(first entry)

AAE17541

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The invention relates to a fluorescent timer protein having an emission CC spectrum that changes over time after synthesis from a first wavelength CC to a second wavelength. The fluorescent timer proteins are useful in CC monitoring the activity of a promoter, determining the age of a protein, CC identifying an agent that modulates the activity of a promoter and in CC enriching a population of cells comprising a fluorescent timer protein. CC The fluorescent timer proteins are also useful for assessing gene CC expression during development of a multicellular organism or during CC cellular differentiation, in response to a drug or other inducer of CC promoter activity, as a reporter to serve as a read-out of promoter CC aspects of the activity of a regulatory element or translocation, CC protein trafficking, or protein stability, to investigate temporal CC visualisation of newly synthesised proteins of accumulated proteins, and CC visualisation of newly synthesised proteins and accumulated proteins, and CC visualisation of newly synthesised proteins and accumulated proteins, and CC techniques are employed, as detectable labels, as selectable markers, as biosensors in prokaryotic and eukaryotic cells, in protease cleavage CC assays, and as second messenger detectors. The nucleic acids can be used CC didications in cell lines. The present sequence is Discosoma sp. ES fluorescent protein derived from humanised wild-type Anthozoa protein CC dirps by substituting Val to Ala at 105 and Ser to Thr at 197
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Val substituted with Misc-difference 197
                                                                                                                                                                                                                                                                                                                                                                       Sequence 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fluorescent timer protein; protein movement; translocation; trafficking; promoter activity; gene expression; transgenic plant; gene modification;
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                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                       Similarity 99.1
23; Conservative
LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60
                                                                                                           MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; 89pp; English.
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                                                                                                                                                                                                                                                                   99.4%;
99.1%;
                                                                                                                                                                                                                                    ; Score 1207; D; Pred. No. 6.3e
                                                                                                                                                                                                                                    DB 5;
5.3e-127;
hes 1;
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Query Match

Score 1207;

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Length 225;

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RESULT 45
ADY51734
                                                                                 to oligomerize. The present invention describes fluorescent proteins derived from naturally occurring green or red fluorescent proteins and provides a fusion protein that comprises a non-oligomerizing fluorescent protein linked to at least one protein of interest. As such, these fusion proteins can be used in methods and compositions to determine the pH of a sample, or whether the sample contains an enzyme, molecule or agent that regulates the activity of an expression control sequence. Furthermore, they may be used to identify a specific interaction of molecules, such that they are useful for improving or developing new assays in the field of molecular biology. This polypeptide sequence is the Discosoma sp. red fluorescent protein (RFP) mutant of the invention. NOTE: This sequence is not given in the invention but it is derived from SeqID 12 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel non-oligomerizing fluorescent protein. Specifically, it refers to the presence of at least one mutation in the fluorescent protein that reduces or eliminates the ability of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New non-oligomerizing fluorescent protein containing at least one mutation that reduces or eliminates the ability of the protein to oligomerize, useful for making better and new assays for molecular
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24-MAY-2001; 2001US-00866538
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Synthetic
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Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page; 117pp; English.
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                                                             information provided
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                                                                in the claims
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RESULT 46
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The invention relates to a non-oligomerising fluorescent protein containing a mutation that reduces or eliminates its ability to oligomerise. The fluorescent protein gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH. These are also used to identify agents or conditions that regulate expression of control sequences. The present sequence is Discosoma sp. red fluorescent protein (RFP) mutant. Note: This sequence is not shown in the specification, however this sequence is constructed based on Discosoma sp. wild-type RFP protein shown in page 30-31 (ABM00918)
                                                                                                                                                                        Fluorescent proteins containing a mutation that reduces or eliminates ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 red
                                                                                                                                                                                                                                                    Tsien RY,
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                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001US-00794308
                                                                                                                                                                                                                                                                          (TSIE/) TSIEN R Y.
(ZACH/) ZACHARIAS (BAIR/) BAIRD G S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                            ZACHARIAS D
BAIRD G S.
                                                                                                                                     3, Page, Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                              or sample pH
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cent protein; RPP; mutant;
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RESULT 47
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                   The invention relates to a non-oligomerising fluorescent protein containing a mutation that reduces or eliminates its ability to oligomerise. The fluorescent protein gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH. These are also used to identify ...
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(ZACH/) ZACHARIAS D
(BAIR/) BAIRD G S.
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                                                                                                                                                               Page; Opp; English.
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Pred. No. 6.3e-127;
D; Mismatches 1;
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expression

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RESULT 48
AD146222
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XX red f
XX Oligo
XX VOLIGO
XX OLIGO
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Best Local S
Matches 224
The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced
                                                                                                                                                                                                                                                                                                                               New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, usefin molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is Discosoma sp. Note: This sequence is not shown i sequence is constructed based on E shown in page 30-31 (ABW00918)
                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 20; 166pp; English
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29-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campbell RE,
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Conservative
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Pred. No. 6.3e-127;
0; Mismatches 1;
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\texttt{CXSS} \times \texttt{PPPP} \times \texttt{XSPXPSP} \times \texttt{PXSPXPXPSP} \times \texttt{PPPPXXPXPSP} \times \texttt{PXSPXPSP} \times \texttt{PXSPXPSP} \times \texttt{PXSPXPSP} \times \texttt{PXSPSP} \times \texttt{PX
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               propensity for oligomerization, especially tetramerization. The protes may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABW00933
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                                                                                                                                                                            Fluorescent proteins containing a mutation that reduces or eliminates i ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                           Tsien RY,
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                                                                         Example 2; Page;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TSIE/) TSIEN R Y.
(ZACH/) ZACHARIAS D A.
(BAIR/) BAIRD G S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001US-00794308
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Pred. No. 6.3e-127;
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The invention relates to a non-oligomerising

fluorescent protein

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RESULT 50
ABW00934
ID ABW000
XX ABW000
XX ABW000
XX Disco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is constructed based on Discosoma sp. wild-type RFP protein shown in page 30-31 (ABW00918)
                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001US-00794308
                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001US-00794308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fluorescent protein; resonance energy
red fluorescent protein; RFP; mutant;
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Fluorescent proteins containing a mutation that reduces or eliminates its ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH.
                                                                                                                                                                                                                                                                   (TSIE/)
                                                                                                                                       WPI; 2003-802418/75.
                                                                                                                                                                                                                                           (BAIR/)
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                                                                                                                                                                                                                                           ) TSIEN R Y.
) ZACHARIAS D A.
) BAIRD G S.
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                                                                                                                                                                                         Zacharias
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    red fluorescent protein (RFP), K83W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Lys is substituted with Trp"
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Pred. No. 8.2e-127;
0; Mismatches 1;
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RBSULT 51
ADH34501
ID ADH34501
XX ADH34501
XX DH33
XX DI 11-MJ
XX Chror
KW Chidu
KW Chidu
KW Chidu
KW Iluo
KW Filuo
KW Filuo
KW Filuo
KW Filuo
KW Wholl
KW End i
KW Syntl
OS Disc
XX Syntl
OS Disc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidnarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable marker; sunscreen; selective filter; fluorescence resonance energy transfer; FRET; biosensor; whole cell marker; second messenger detector; in vivo marker; fluorescence activated cell sorting; fluorescent timer; red fluorescent protein; DsRed; mutant; mutein.
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                                                                                                                                                                                                                                                                                        Misc-difference
  26-DEC-2001; 2001US-0343128P
                                                           23-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Discosoma
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                                                                                                                 17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                           2002WO-US041418
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                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  /note= "Ala replaces
residue 148"
                                                                                                                                                                                                                                  /note= "Met replaces wild-type Lys.
residue 167"
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99.6%;
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Pred. No. 8.2e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                      wild-type Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 225;
                                                                                                                                                                                                                                                                   Corresponds to
                                                                                                                                                                                                                                                                                                                                                         Corresponds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC analyte detection assays as selectable markers in recombinant DNA
CC applications (e.g. the production of transgenic cells and organisms), and
CC are also useful as sunscreens and selective filters. Chromoprotein
CC mutants having fluorecent protein activity useful in fluorescence
CC resonance energy transfer (FRET) applications, as biosensors in
CC protearyotic and eukaryotic cells, as markers of whole cells to detect
CC changes in multicellular reorganisation and migration, as second
CC messenger detectors, as in vivo markers in animals (e.g., transgenic
CC animals), in fluorescence activated cell sorting applications, in
CC protease cleavage assays and in assays to determine the phospholipid
CC composition in biological membranes. Proteins with fluorescent protein
CC activity can also be used as fluorescent timers, where the switch of one
CC activity can also be used as fluorescent timers, where the switch of one
CC the ageing of the protein and is useful for determination of the
CC the ageing of the protein and is useful for determination of the
CC cativation or deactivation of gene expression. The present sequence
CC represents a Discosoma sp. red fluorescent protein bared mutant generated
CC in an example of the invention. The present sequence is not shown in the
CC protein and the invention of the wild-type bared sequence.
CC protein the protein and the information protein bared as
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to those found in a chromoprotein is therefore proposed to confer chromoprotein activity on the fluorescent protein mutant, with chromoproteins being able to be converted into fluorescent proteins in a similar manner. The invention also relates to expression constructs, vectors, host cells and host cell progeny comprising a nucleic acid of the invention; the recombinant production of an interconverted chromoprotein or fluorescent protein mutant; and antibodies specific for interconverted mutant proteins of the invention. The interconverted mutants are useful in any application that employs a chromoprotein or fluorescent protein. Fluorectin protein mutants having chromoprotein activity can useful as colouring agents in, for example, food compositions, pharmaceuticals, cosmetics and living organisms. Proteins with chromoprotein activity are also useful as labels in biological than the content of the content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chidarian species, and most preferably an Anthozoan species. The invention is based on the finding that although green fluorecent protein (GFP)-like chromoproteins and fluorescent proteins exhibit some degree of homology, there are certain positions (referred to as 148, 165, 167 and 203; numbering corresponds to GFP) that are occupied by noticeably different residues in the two types of proteins. Mutagenesis of the residues in these key positions in, for example, a fluorescent protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to interconverted mutants of chromoproteins (CP) or fluorescent proteins (FP) and nucleic acids encoding them. The mutant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bulina ME,
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                     121
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                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                          LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
          KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                               MRSSKNVIKEFMRFKVRMEGTVNGHBFEIBGBGGRPYEGHNTVKLKVTKGGPLPFAMDI
                                                                                                                                                                                                                     MRSSKNVIKEFMRFKVRMEGTVNGHBFBIEGBGBGRPYBGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shown in
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                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 1 and
                                                                                                                                                                                                                                                                                                                                                                                      99.3%;
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                                                                                                                                                                                                                                                                                                                                                       Score 1205; DB 7;
Pred. No. 1.1e-126;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           provided
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           page 42.
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RESULT 52
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protein (I) comprising a 241 residue amino acid sequence (see ABP5678, 51), with one or more point mutations at amino acid sequence (see ABP5678, K164, or M183. Also described: (1) a fusion protein comprising (I); (2) an isolated nucleic acid encoding (I); (3) a vector comprising the nucleic acid of (2); (4) a host cell comprising the vector; (5) a retroviral cDNA expression library comprising the nucleic acid of (2), or encoding (I); and (6) methods of making a fluorescent variant. The Discosoma red fluorescent proteins are useful for functional screens as a reporter for gene transcription (e.g. as a fusion protein), for target characterisation and localisation of fusion proteins, or for scaffolds for protein and peptide libraries. The fluorescent proteins can also be used as selectable markers or reporter molecules for a variety of bioassays, including methods that use fluorescence activated cell sorting (FACS) as a selection mechanism. The method of directed protein evolution
                                                                                                                                                                                                                                                                                            New Discosoma red fluorescent protein, useful for functional screens as a reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-2002; 2002WO-US015968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                 The present invention describes an isolated Discosoma red fluorescent
                                                                                                                                                                                                                                               Claim 1; Fig 1;
                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABZ22476.
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-120798/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-2001; 2001US-0291871P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                              22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "possible mutations at this point F125V" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "possible mutations at this point are N24S, and N24H" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  optimised Discosoma red fluorescent protein; Discosoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "encoded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC"
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RESULT 53
AAB22923
ID AAB229
XX AAE28
AC AAE28
AC AAE28
XX Fluor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; NFP-6; mutant;
                                                                                                                                                                                                                                                                                                       06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                     20-FEB-2002; 2002WO-US005749
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04-DEC-2001; 2001US-00006922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                           Lukyanov S,
                                                                                                                             (CLON-) CLONTECH LAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 225
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                                                                           Lukyanov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drFP583 (NFP-6) mutant protein, E83 (N42H+V71A+I180H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                        Disclosure; Page; 80pp;
                                                                                                                                                         English.
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chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sumscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drFP583 (NFP-6) wild-type protein shown as SEQ ID NO:8 (AAE28833) in page 70-71 of the specification The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are 225 B

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                                                   KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSV
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RESULT 54
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Pluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drPP583 protein; NFP-6; mutant;
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                                         Misc-difference
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                                                                                                                                                                                                                              drFP583 (NFP-6) mutant protein,
                                                                                  Location/Qualifiers
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                                                                                  Pluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay;
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2001US-00006922.
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RESULT 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding a of an aggregating Cnidarian analyte detection assays or
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04-DEC-2001; 2001US-00006922
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                                                                                                                                                                                     LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                      MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                         YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                      KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                             LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVATVTQDSSLQDGCFIY
                                                                                                                                                                                                                                               MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                            225 AA;
                                                                              KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGETHKALKLKDGGHYLVEFKSI
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lukyanov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yanushevich
                                                                                                                                                                                                                                                                                                                           Score 1202; D
Pred. No. 2.3e
1; Mismatches
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chromo- or fluorescent p
fluorescence activated of
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                                                                                                                                                                                                                                                                                                                                            DB 5;
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                                                                                                                                                                                                                                                                                                                                                                  Length
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    or fluorescent mutant
protein or mutant for
cell sorting

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                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                120
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The invention relates to interconverted mutants of chromoproteins (CP) or cluorescent proteins (FP) and nucleic acids encoding them. The mutant is CC derived from a Chidnarian species, preferably a non-bioluminescent CC invention is based on the finding that although green fluorescent protein (GFP) like chromoproteins and fluorescent proteins exhibit some degree of CC (GFP) like chromoproteins and fluorescent proteins exhibit some degree of CC (GFP) like chromoproteins and fluorescent proteins exhibit some degree of CC (GFP) like chromoproteins and fluorescent proteins exhibit some degree of CC (GFP) like chromoproteins and fluorescent proteins exhibit some degree of CC (GFP) like chromoprotein some degree of CC (GFP) like chromoprotein some degree of CC (GFP) like chromoprotein the two types of proteins. Mutagenesis of the CC (GFP) like a fluorescent protein in a chromoprotein activity on the fluorescent protein mutant, with CC (Chromoprotein activity on the fluorescent protein mutant, with CC (Chromoprotein or liverion also relates to expression constructs, CC (Chromoprotein or fluorescent protein mutant; and antibodies specific for interconverted mutant proteins of the invention. The interconverted mutants are useful as colouring agents in, for example, food compositions, pharmaceuticals, cosmetics and living organisms. Proteins with Chromoprotein activity are also useful as labels in biological CC analyte detection assave, as selectable markers in recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidnarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable muscreen; selective filter; fluorescence resonance energy transfer; FRET; biosensor; whole cell marker; second messenger detector; in vivo marker; fluorescence activated cell sorting; fluorescent timer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid encoding in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; 'Page; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bulina ME, Chudakov D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2001; 2001US-0343128P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-2002; 2002WO-US041418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fluorescent protein which
analyte detection assays, as selectable markers in recombinant DNA applications (e.g. the production of transgenic cells and organisms), are also useful as sunscreens and selective filters. Chromoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CLON-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fluorescent protein; DsRed; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-607998/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gp.
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residue 165"
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Ala replaces wild-type Ser.
residue 203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lukyanov KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interconverted mutant of chromo-or re useful as biosensors, coloring agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corresponds to
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RESULT 57
ADH34502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, as markers of whole cells to detect changes in multicellular reorganisation and migration, as second messenger detectors, as in vivo markers in animals (e.g., transgenic animals), in fluorescence activated cell sorting applications, in protease cleavage assays, and in assays to determine the phospholipid protease cleavage assays, and in assays to determine the phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composition in biological membranes. Proteins with fluorescent protein activity can also be used as fluorescent timers, where the switch of one fluorescent colour to another (e.g., green to red) is concomitent with the ageing of the protein and is useful for determination of the activation or deactivation of gene expression. The present sequence represents a Discosoma sp. red fluorescent protein DsRed mutant generated in an example of the invention. The present sequence is not shown in the specification, but was derived from the wild-type DsRed sequence
                                                                                                                                                                                                                                                                                                                                             Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidnarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable marker; sunscreen; selective f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutants having fluorecent protein activity useful
                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                   Discosoma вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH34502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH34502 standard; protein; 225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                       Misc-difference
                                                                                                                                                                                                                            Discosoma
                                                                    Misc-difference
                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                            whole cell marker; second messenger detector; in vivo marker; fluorescence activated cell sorting; fluorescent timer;
                                                                                                                                                                                                                                                                                                                              fluorescence resonance energy transfer; FRET; biosensor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ADH34489) shown in Fig 1 and the information provided on page
                                                                                                                                                                                                                                                                               fluorescent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVKFIGVNFPSDGPVMQKKTMGWEAATERLYPRDGVLKGESHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     DsRed mutant S148A/K167M/S203A.
                                                                    197
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                             protein; DsRed; mutant; mutein.
                                                                                     /note= "Met replaces wild-type Lys.
residue 167"
                                                                                                                       163
                                                                                                                                       /note= "Ala replaces wild-type Ser.
residue 148"
                                      residue
                                    /note= "Ala replaces wild-type Ser.
residue 203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.0%;
98.7%;
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Pred. No. 2.3e-126;
Pred. No. 2.3e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                           Corresponds to GFP
                                                        Corresponds to GFP
                                                                                                         Corresponds
                                                                                                                                                                                                                                                                                                                                                      selective filter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225
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WO2003057833-A2

Bulina ME,

Chudakov D,

Lukyanov KA

26-DEC-2001; 2001US-0343128P.

(CLON-) CLONTECH LAB INC

23-DEC-2002; 2002WO-US041418.

17-JUL-2003

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                                                                                                                                                                                                                                                The invention relates to interconverted mutants of chromoproteins (CP) or CP (Iluorescent proteins (FP) and nucleic acids encoding them. The mutant is CP chidarian species, and most preferably an Anthozoan species. The mutant is CP (Cidarian species, and most preferably an Anthozoan species. The control is based on the finding that although green fluorescent protein (CPP) like chromoproteins and fluorescent proteins exhibit some degree of CPP) like chromoproteins and fluorescent proteins exhibit some degree of CPP (1) like chromoproteins and fluorescent proteins exhibit some degree of CPP) that are occupied by noticeably CPP (1) in the two types of proteins exhibit some degree of CPP (1) like chromoprotein in for example, a fluorescent protein, control con
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                       fluorescent colour to another (e.g., green to red) is concomitant with the againg of the protein and is useful for determination of the activation of gene expression. The present sequence represents a Discosoma sp. red fluorescent protein DsRed mutant generated in an example of the invention. The present sequence is not shown in the specification, but was derived from the wild-type DsRed sequence (ADH34489) shown in Fig 1 and the information provided on page 42.
                                                                                                                                                                                                                                              Sequence 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page; 56pp; English.
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                                                                                                                                                                             Local
                         13
                                                                                                                                                                               Similarity
LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                     MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60
                                                                                              MRSSKNVIKEFMRFKVRMEGTVNGHEFBIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60
                                                                                                                                                          Conservative
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                                                                                                                                                                               99.0%;
                                                                                                                                                        2
                                                                                                                                                        Score 1202; DI
Pred. No. 2.3e
2; Mismatches
                                                                                                                                                                               .3e-126;
                                                                                                                                                                                                    DB 7;
                                                                                                                                                                                                    Length 225;
                                                                                                                                                        Indels
                                                                                                                                                        0
                                                                                                                                                      Gaps
                         120
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Sequence 240 AA;

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RESULT 58
CC protein (1) comprising a 241 residue amino acid sequence (see ABB5678, CC S1), with one or more point mutations at amino acid sequence (see ABB5678, CC X164, or M183. Also described: (1) a fusion protein comprising (1); (2) CC an isolated nucleic acid encoding (1); (3) a vector comprising the comprision for target compression and comprising the comprision protein, or for target compression, and localisation of fusion proteins, or for target compression, and/or folding that use fluorescent protein can also be compactly for compression, and/or folding kinetics as compared to wild type correspond to potentiased variant. The present sequence represents a mammalian correspond to potentianed variant. The present sequence is not given in the consistent of bicosoma red fluorescent protein variant from the compact to wild type correspond to the compact of the compact of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated Discosoma red fluorescent protein (I) comprising a 241 residue amino acid sequence (see ABP5667)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Discosoma red fluorescent protein, useful for functional screens as a reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-2001; 2001US-0291871P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-2002; 2002WO-US015968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fluorescent protein variant K93R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22pp; English.
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Length 240;

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Best Local Similarity
The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant
                                                                                                                                        Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous
                                                                                                                                                                                                                  Jones EL, Kare
Hoegh-Guldberg
                                                                                                                                                                                                                                                                                                           02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002; 2002WO-GB000928
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                                                                                                                                                                                                                                                                                                                                                                                                                  WO200270703-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
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22-JAN-2003
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                                                                                                     Example
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                                                                                                                                                                                                                                                          NUFARM LTD.
UNIV QUEENSLAND.
JONES E L.
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                                                                                                                                                                                                                    Karan M,
berg IO,
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(first en
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                                                                                                     499;
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98.7%;
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Prescott M;
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Pred. No. 2.5e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CFM)
                                                                                                    English
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RESULT 60
AAE28926
ID AAE28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc extracts, e.g. flavouring, beverage or juice or colouring agent. Other cuses include transducing or intensifying an image, providing additional clight for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car cy upholstery. CPMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, corans are useful in the colour in contemplated uses include, cin sunscreens. CPMs modify visible colour in edible and/or ornamental cc fungal species, and in fruits and vegetables to enhance their companies, and in fruits and vegetables to enhance their contemplated uses of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CPM related amino critical sequences. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; NFP-6; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 225 AA;
                                                                                                                                                                                                                                                   Discosoma
Synthetic
                                                                                                                                                                                                                                                                                                   mutein
                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE28926 standard; protein;
                                                                                                         Misc-difference
                                                                                                                                          Misc-difference
                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                     Misc-difference
                                                            WO200268459-A2
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                                                                                                                                                                                                                                                                                                                                                                                                             drFP583 (NFP-6) mutant protein, (V71M+V105A+Y120H+S197T).
                                                                                                                                                                      /note=
                                                                                                           /note=
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                            120
                                                                                                                                                         note=
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98.7%;
                                                                                                                         "Wild-type
                                                                                                                                                                                      "Wild-type Val
                                                                                            "Wild-type
                                                                                                                                                         "Wild-type
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Pred. No. 3.9e-126;
                                                                                             Ser
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20-FEB-2002; 2002WO-US005749

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RESULT 61
ADH34505
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Synthetic.
Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drrP583 (NFP-6) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drrP583 (NFP-6) wild-type protein shown as SEQ ID NO:8 (AAEZ8833) in page 70-71 of the specification
                                                                                                        Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidnarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable marker; sunscreen; selective filter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding a of an aggregating Cnidarian analyte detection assays or
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04-DEC-2001;
                                                red
                                                             whole cell marker; second messenger detector; in vivo marker;
fluorescence activated cell sorting; fluorescent timer;
                                                                                                                                                                                                      11-MAR-2004
                                                                                                                                                                                                                                      ADH34505
                                                                                                                                                                                                                                                                ADH34505 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page; 80pp; English
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                                                                                            fluorescence resonance energy transfer; FRET; biosensor;
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                                                                                                                                                                                                                                                                                                                                                                                                                           KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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2001US-00006922.
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                                                                                                                                                                       mutant S148C/I165N/S203A.
                                                                                                                                                                                                      entry)
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98.2%;
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chromo- or fluorescent p
fluorescence activated of
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Pred. No. 5e-126;
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cell sorting
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Compositions proteins and recorded to as 148, 165, 167 and considered to different residues in the two types of proteins. Mutagenesis of the contered to those found in a chromoprotein is therefore proposed to confer consorprotein activity on the fluorescent protein mutant, with consorprotein activity on the fluorescent protein mutant, with consorprotein so the invention also relates to expression constructs, converted manner. The invention also relates to expression constructs, converted mutant proteins of the invention. The interconverted conference the invention of an interconverted interconverted mutant protein of an interconverted converted mutant protein of the invention. The interconverted composition in any application that employs a chromoprotein or interconverted mutant proteins of the invention. The interconverted compositions pharmaceuticals, cosmetics and living organisms. Proteins composition in the proteins of the protein activity are also useful as labels in biological and compositions in biological as smarkers and selective filters. Chromoprotein considered the protein activity useful in fluorescence considered to proteins and markers in animals (e.g., transgenic colls and organisms), and composition in biological membranes. Proteins with fluorescence activated cells sorting applications, as second composition in biological membranes and migration, as second composition in biological membranes. Proteins with fluorescent protein considered the protein of the protein activation of the considered cells to detect the considered considered as fluorescent timers, where the switch of one considered considered considered consi
The invention relates to interconverted mutants of chromoproteins (CP) of fluorescent proteins (FP) and nucleic acids encoding them. The mutant is derived from a Chidnarian species, preferably a non-bioluminescent Chidarian species, and most preferably an Anthozoan species. The invention is based on the finding that although green fluorescent protein (GFP)-like chromoproteins and fluorescent proteins exhibit some degree
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Misc-difference
                   in an example of the invention. The present sequence is not shown in specification, but was derived from the wild-type DsRed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid encoding interconverted mutant of chromo-or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-607998/57.
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197
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residue 148"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are useful as biosensors,
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Best Local S
Matches 222
The present invention describes an isolated Discosoma red fluorescent protein (I) comprising a 241 residue amino acid sequence (see ABP56678, S1), with one or more point mutations at amino acid position N24, F125, K164, or M183. Also described: (1) a fusion protein comprising (I); (2) an isolated nucleic acid encoding (I); (3) a vector comprising the nucleic acid of (2); (4) a host cell comprising the vector; (5) a retroviral cDNA expression library comprising the nucleic acid of (2). o encoding (I); and (6) methods of making a fluorescent variant. The Discosoma red fluorescent proteins are useful for functional screens as reporter for gene transcription (e.g. as a fusion protein), for target characterisation and localisation of fusion proteins, or for scaffolds for protein and peptide libraries. The fluorescent proteins can also be
                                                                                                                                                                                                                                          New Discosoma red fluorescent protein, useful for functional screens as a reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptide
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Discosoma; red f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                               PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fluorescent protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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98.7%;
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Pred. No. 5e-126;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          red fluorescent protein; variant; directed evolution; mutant.
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RESULT 63
ABP56683
ID ABP56683
XX ABP56683
AC ABP56
XX Disc
XX Disc
XX Mamma
KW Disc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Discosoma
Synthetic.
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                                                                                                                            New Discosoma red fluorescent protein, useful for functional reporter for gene transcription, for target characterization localization of fusion proteins, or for scaffolds for protein
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                                                                                                         libraries
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98.7%;
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Pred. No. 5.5e-126;
2; Mismatches 1;
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directed evolution; mutant.
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Claim 14;

Page;

22pp;

English.

The present invention describes

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isolated

Discosoma

red

fluorescent

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RESULT 64
ADH34504
ADH34504
XX ADH34
XX ADH34
XX Discr
XX Chron
KW Chick
KW anall
KW fluol
KW fluol
KW fluol
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Best Local S
Matches 222
                                                                                                                                                                                                                                                                             Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidnarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable marker; sunscreen; selective filter; fluorescence resonance energy transfer; FRET; blosensor; whole cell marker; second messenger detector; in vivo marker; fluorescence activated cell sorting; fluorescent timer; red fluorescent protein; DBRed; mutant; mutein.
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                                                                                                                                                                                                                            Synthetic
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                                                                                                                 Location/Qualifiers 146
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                                                         /note= "Ala replaces wild-type Ser. Corresponds residue 148"
     note= "Ser replaces wild-type Ile. Corresponds to
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98.7%;
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Pred. No. 5.5e
2; Mismatches
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Query Match

Score 1196;

BB

Length 225

Sequence

225 AA;

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CC different residues in the two types of proteins Mutagenesis of the CC residues in these key positions in, for example, a fluorescent protein, CC to those found in a chromoprotein is therefore proposed to confer CC chromoproteins being able to be converted into fluorescent proteins in a CC chromoproteins being able to be converted into fluorescent proteins in a CC chromoprotein or fluorescent protein mutant, with the recombinant protein mutant protein constructs, the invention also relates to expression constructs of the invention; the recombinant protein mutant; and antibodies specific for CC chromoprotein or fluorescent protein mutant; and antibodies specific for interconverted mutant protein protein mutant; and antibodies specific for fluorescent protein mutant; and antibodies specific for conjunction are useful as colouring agents in, for example, food compositions, pharmaceuticals, cosmetics and living organisms. Proteins CC compositions (e.g. the production of transgenic cells and organisms), and CC analyte derection assays, as selectable markers in recombinant DNA CC applications (e.g. the production of transgenic cells and organisms), and CC analyte derectors, as in exposition activity useful in fluorescence cells as markers of whole cells to detect changes in multicellular reorganisation and migration, as second CC animals), in fluorescence protein activity useful in fluorescence cells as in vivo markers in animals (e.g., transgenic cells and in biological membranes. Proteins with fluorescent protein cells and migration, as second cells composition in biological membranes. Proteins with fluorescent protein cells and in assays to determinate the phospholipid cells and in biological membranes. Proteins with fluorescent protein cell cells in an example of the protein and is useful for determination of the switch of one cells fluorescent protein Darkd mutant generated cell and in assays to determination of the membranes. Protein bardd mutant generated cell and fluorescent protein bardd mutant generated i
(GFP)-like chromoproteins and fluorescent proteins exhibit some degree homology, there are certain positions (referred to as 148, 165, 167 and 203; numbering corresponds to GFP) that are occupied by noticeably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to interconverted mutants of chromoproteins (CP) fluorescent proteins (FP) and nucleic acids encoding them. The mutant iderived from a Chidnarian species, preferably a non-bioluminescent Chidarian species, and most preferably an Anthozoan species. The invention is based on the finding that although green fluorecent protein the content of the content protein the 
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Matches
The invention describes a first mutant fluorescent protein (I) comprising an amino acid sequence that differs from that of a corresponding wild-type red fluorescent protein by an amino acid substitution, where the first mutation fluorescent protein mutant has an optical property that differs relative to the corresponding optical property produced by the wild-type red or green fluorescent protein. (I) is useful for detecting expression of gene. The polynucleotide (II) encoding (I) is useful for detecting expression of a gene which involves introducing (II) into a cell or organism, allowing the cell to replicate, and detecting expression of the nucleic acid by emission of fluorescent light. The expression of the nucleic acid expression is detected in vivo or in
                                                                                                                                                                                                                                                                                                                                                                                                                          New first mutant fluorescent protein having an optical property relatively different to a corresponding optical property produced by wild-type red or green fluorescent protein, useful for detecting expression of a gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMAKKPVQLPGYYYVDSKLDITSHNKDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anemone.
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                                                                                                                                               Carter RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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98.2%;
                                                                                                                                                     Schmale
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New first mutant fluorescent

protein having

an optical property

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RESULT 67
ADZ84223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC differs relative to the corresponding optical property produced by the CC wild-type red or green fluorescent protein. (I) is useful for detecting expression of gene. The polynucleotide (II) encoding (I) is useful for detecting expression of a gene which involves introducing (II) into a CC cell or organism, allowing the cell to replicate, and detecting CC expression of the nucleic acid by emission of fluorescent light. The CC expression of the nucleic acid expression of fluorescent light. The CC expression of the nucleic acid expression is detected in vivo or in CC which contains (II). (I) is useful as a marker for detecting expression of a gene, in blochemical assays, and as reagents. (I) is also useful in CC multiple labeling systems, as in vivo markers such as in mRNA CC microinjection assays, and as taxonomic markers for studies of genetics, CC colour indicators in diagnostic kits, coloured food additives, and CC commetics ingredients. (I) is useful in research for up or down CC regulation, to monitor promoter activity, to allow longer term monitoring CC and to localise proteins. (I) has enabled properties such as CC amino acid sequence of RedII, a mutant of the red fluorescent protein CC isolated from an aquatic species believed to be either an Actinodiscus or CC consections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                Corallimorpharia
                                                                                                                                                                                               Actinodiscus/Discosoma RFP mutant Red I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relatively different to a corresponding optical property produced by wild-type red or green fluorescent protein, useful for detecting expression of a gene.
                                      Misc-difference
                                                                                                                                                    Red fluorescent protein;
                                                                                                                                                                                                                                      14-JUL-2005
                                                                                                                                                                                                                                                                            ADZ84223
                                                                                                                                                                                                                                                                                                               ADZ84223 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; SEQ ID NO 4; 30pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a first mutant fluorescent protein (I) comprising an amino acid sequence that differs from that of a corresponding wild-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ype red fluorescent protein by an amino acid substitution, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60
                                                                                                                                                                                                                                                                                                                                                                                                               YMAKKPVQLPGYYYVDSKLDITSHNKDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSCSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   species.
                                                                                                                                                                                                                                      (first entry)
                                    Location/Qualifiers
/note= "This residue is Asn in the mutant Ac/DsRFP Red II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.5%;
                                                                                                                                                        Red I; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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Pred. No. 1.2e-125;
2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                Matches 221;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel mutant fluorescent protein comprising amino acid sequence that differs from wild-type red or green fluorescent protein by amino acid substitutions, useful as markers for detecting desired gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represents the mutant Actinodiscus/Discosoma red fluorescent protein Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; SEQ ID NO 2; 29pp; English
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(CART/) CARTER R W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCHM/) SCHMALE M C.
                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
181
                                          181
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                                                                                                                                                                                                               LSPQPQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                          YMAKKPYOLPGYYYYDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                 KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                         MSCSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGFLPFAWDI
                                                                                         KVKF1GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE1HKALKLKDGGHYLVEFKT1
                                                                                                                                                                              LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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98.2%;
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                                                                                                                                                                                                                                                                                                                                                              Score 1196; DB 9;
Pred. No. 1.2e-125;
o. Mismatches 2;
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RESULT 68
ADZ84225
The invention relates to mutant red and green fluorescent proteins which CC have higher fluorescent intensities compared to the wild-type proteins CC encoding the mutant fluorescent proteins, and transgenic animals CC comprising such a nucleic acid. The mutant red fluorescent proteins (RFP) CC of the invention, Red I (ADZ84223) and Red II (ADZ84225), are derived CC from a novel wild-type RFP (referred to as AC/DSRP) isolated from a CC mushroom coral believed to be either an Actinodiscus or Discosoma CC (ADZ84227) and Green (ADZ84223) are derived from a believed to be either an Actinodiscus or Discosoma CC (ADZ84227) and Green (ADZ84229), are derived from a invent wild-type GFP (known as McGFP) isolated from the great star coral Montastrace CC wild-type Ac/DsRPP and McGFP cDNAs to low-stringency PCR to introduce CC wild-type Ac/DsRPP and McGFP cDNAs to low-stringency PCR to introduce CC wild-type Ac/DsRPP and McGFP cDNAs to low-stringency PCR to introduce CC mutant fluorescent proteins of the PCR products into bacterial expression CC fluorescence compared to those expressing the wild-type proteins. The CC fluorescence compared to those expressing the wild-type proteins. The CC fluorescence compared to those expressing the wild-type proteins. The cCC of applications. They are useful as markers for detecting the expression of a gene of interest, or can be used as in vivo markers in mRNA CC misconjection assays in transgenic animals. They can be used in Edward assays and as reagents. CC crepresents or can be used as in vivo markers for studies of condarian genetics, as color indicators in diagnostic kits, as colored CC represents and as cosmetic ingredients. The present sequence CC represents enhanced condariants are found to have a fluorescent intensity at least 50% greater than the mutant RFP Red I (ADZ84223).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel mutant fluorescent protein comprising amino acid sequence that differs from wild-type red or green fluorescent protein by amino aci substitutions, useful as markers for detecting desired gene expressi
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; SEQ ID NO 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-DEC-2002; 2002US-00314936
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CARTER R W.
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Best Local
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07-FEB-2000; 2000US-00499464.
24-WAY-2002; 2000US-00154758.
29-JAN-2003; 2003US-00353090.
09-APR-2003; 2003US-0461133P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecular interaction detection; biomolecular interaction detection; fluorescent protein; multi-colour PCA; drug discovery; target validation; high-throughput screening; high-content screening; pathway mapping; drug mechanism-of-action study; biosensor; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ59562
The invention describes a composition (I) comprising complementary fragments of a protein or mutant protein, where the fragments generate optically detectable signal when associated, and each of the mutant protein fragments is fused to a separate molecule. Also described are:
                                                                                                                                                                                                 Composition useful in protein fragment complementation assays for drug discovery and high-throughput screening, comprising complementary fragments of protein or mutant protein, generating optically detectable
                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2003; 2003US-00724178.
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                                                                                                                                                                                                                                                                                                                                                                                                     (MACD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fluorescent
                                                                                                                              Disclosure; SEQ ID NO 12; 34pp; English.
                                                                                                                                                                               signal when associated.
                                                                                                                                                                                                                                                                                                                                                    Watson Michnick SW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICH/)
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MACDONALD M L.
LAMERDIN J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSCSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detectable signal;
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                                                                                                                                                                                                                                                                                                                                                       Macdonald
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein fragment complementation assay; ion; biomolecular interaction detection;
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                                                                                                                                                                                                                                                                                                                                                         Lamerdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        optically detectable protein separately to other molecules, reassociating the protein fragments through interactions of the molecules that are fused or attached to the fragments, and detecting the resulting optical signal; designing and engineering of PCAs based on fluorescent protein; and a method and composition for the construction of multi-color PCAs.

(I) is useful in PCAs and other assays for drug discovery, target validation, high-throughput screening, high-content screening, pathway mapping, drug mechanism-of-action studies, biosensors and disgnostics.

(I) is useful for engineering different colour PCAs for a variety of applications in biology and biotechnology. This is the amino acid fluorescent proteins with Asquores green flourescent protein, variants of which can be created with Asquores green flourescent protein, variants of relative to wild type GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions, involving reassembling separate fragments from an optically detectable protein, and detecting the reassembly by units of reconstitution of activity of the optically detectable protein, where the reassembly of the fragments is operated by the interaction of molecular domains fused to each fragment, and is independent of other molecular processes; detecting biomolecular interaction, involving selecting an appropriate optically detectable protein, effecting fragmentation of the optically detectable protein such that the fragmentation results in reversible loss of protein function, fusing or attaching fragments of the
                                          18-MAY-2001; 2001US-0291871P
                                                                                  20-MAY-2002; 2002WO-US015968.
                                                                                                                                                                 WO200294992-A2
                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                              Discosoma
                                                                                                                                                                                                                                                                     Discosoma; red
                                                                                                                                                                                                                                                                                                                                  Discosoma
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    (RIGE-) RIGEL PHARM INC
                                                                                                                           28-NOV-2002
                                                                                                                                                                                                                                                                                          Mammalian codon optimised Discosoma red fluorescent protein; variant;
                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                   ABP56681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP56681 standard; protein;
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                                                                                                                                                                                                                                                                                                                                red fluorescent protein variant F125L and
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                                                                                                                                                                                                                                                                   fluorescent protein;
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Pred. No. 1.8e-125;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                     evolution; mutant
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The present invention describes an isolated Discosoma red fluorescent CC protein (I) comprising a 241 residue amino acid sequence (see ABP56678, CC S1), with one or more point mutations at amino acid sequence (see ABP56678, CC K164, or M183. Also described: (1) a fusion protein comprising (1); (2) CC an isolated nucleic acid encoding (I); (3) a vector comprising the cc mucleic acid of (2); (4) a host cell comprising the vector; (5) a CC retroviral cDNA expression library comprising the nucleic acid of (2), or CC encoding (I); and (6) methods of making a fluorescent variant. The CC Discosoma red fluorescent proteins are useful for functional screens as a CC reporter for gene transcription (e.g. as a fusion protein), for target CC for protein and localisation of fusion proteins, or for scaffolds (for protein and localisation of fusion proteins, or for scaffolds (2) to see a selectable markers or reporter molecules for a variety of CC used as selectable markers or reporter molecules for a variety of CC used as selection mechanism. The method of directed protein evolution (2) wariants of Discosoma red fluorescent protein have greatly improved CC variants of Discosoma red fluorescent protein have greatly improved CC brightness, expression, and/or folding kinetics as compared to wild type or a codon optimised Discosoma red fluorescent protein represents a mammalian CC codon optimised Discosoma red fluorescent protein have greatly improved cor a codon optimised Discosoma red fluorescent protein have greatly improved cor a codon optimised Discosoma red fluorescent protein have greatly improved cor a codon optimised Discosoma red fluorescent protein have greatly improved cor a codon optimised Discosoma red fluorescent protein have greatly improved cor a codon optimised Discosoma red fluorescent protein have greatly improved cor a codon optimised Discosoma red fluorescent protein have greatly improved corescent invention. N.B. The present sequence is not given in the greatly discosoma red fluorescent protein will the cor
Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Discosoma red fluorescent protein, useful for functional screens as a reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-120798/11.
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Best Local :
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                                                                                                                                                                                                                                 Similarity
                                                                                                                         LSPOFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                           MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVIKGGPLPFAWDI
YMAKKPVQLPGYYYVDSKLDITSHHEDYTIVEQYERTEGRHHLFL
              YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                    KVKLIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                    KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                               VRSSKNVIKEFMRFKVRMEGTVSGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                           LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                              98.4%;
                                                                                                                                                                                                               3
                                                                                                                                                                                                                                Score 1194; DB 6
Pred. No. 2e-125;
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                             Length 240;
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                                                                                                                                                                                                                    Gaps
                                                      181
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RESULT 71
ADH34506
ID ADH34
XX ADH34
XX ADH34
XX II-MP
XX Disc
XX Chrom
KW Chrom
KW Chrom
KW anally
KW fluot
                   Chromoprotein; fluorescent protein; CP; FP; interconverted mutant; Cnidnarian; Anthozoan; labelling; colouring agents; pigment; analyte detection assay; selectable marker; sunscreen; selective f
                                                                                                                                 11-MAR-2004
                                                                                                                                                                      ADH34506;
                                                                                                                                                                                                         ADH34506 standard; protein; 225 AA.
                                                                                           gg.
                                                                                                                                 (first entry)
                                                                                             DaRed mutant DaRed-NF S148C/I165N/K167M/S203A
                       selective filter;
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resonance energy transfer;

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CC (GFP)-like chromopyroteins and fluorescent proteins whibit some degree of CC (GFP)-like chromopyroteins to GFP) that are occupied by noticeably CC different residues in the two types of proteins. Mutagenesis of the CC residues in these key positions (referred to as 148, 165, 167 and CC of those found in a chromopyrotein is therefore proposed to confer CC tromopyrotein activity on the fluorescent protein mutant, with CC chromopyrotein activity on the fluorescent protein mutant, with CC elimber of the invention also relates to expression constructs, CC vectors, host cells and host cell progeny comprising a nucleic acid of the invention, the recombinant production of an interconverted cC chromopyrotein or fluorescent protein mutant; and antibodies specific for CC chromopyrotein or fluorescent protein mutant; and antibodies specific for CC chromopyrotein or fluorescent protein mutant; and antibodies specific for CC chromopyrotein or fluorescent protein mutant; and antibodies specific for CC chromopyrotein protein fluorescent protein mutants; and antibodies specific for CC chromopyrotein protein activity as a colouring agents in, for example, food compositions, pharmaceuticals, cosmetics and living organisms. Proteins CC with chromopyrotein activity are also useful as sunscreens and selective filters. Chromopyrotein CC analyte detection assays, as selectable markers in recombinant DNA are also useful as sunscreens and selective filters. Chromopyrotein CC mutants having fluorescent protein activity useful in fluorescence cells and organisms), and are also useful as sunscreens and selective filters. Chromopyrotein CC changes in mutalicellular recorganisation and migration, as second cells and inventions, as in vivo markers in animals (e.g., transgenic cells animals), in fluorescence activated cell sorting applications, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to interconverted mutants of chromoproteins fluorescent proteins (FP) and nucleic acids encoding them. The mutaderived from a Chidnarian species, preferably an on-bioluminescent Chidarian species, and most preferably an Anthozoan species. The invention is based on the finding that although green fluorecent provention is based on the finding that although green fluorecent provention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding interconverted mutant of chromo-or fluorescent protein which are useful as biosensors, coloring agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2001; 2001US-0343128P
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fluorescence activated cell sorting; fluorescent timer;
red fluorescent protein; DsRed; non-fluorescent mutant; DsRed-NF; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page; 56pp; English.
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residue 167"
197
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residue 148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Asn replaces wild-type Ile.
residue 165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Ala replaces wild-type
residue 203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lukyanov KA;
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RESULT 72 ABP56679 밁 S 밁 Ś 밁 Ś ននិនិនិនិនិនិនិនិនិនិនិ 밁 8 Query Match Best Local ( Matches protease cleavage assays, and in assays to determine the phospholipid composition in biological membranes. Proteins with fluorescent protein activity can also be used as fluorescent timers, where the switch of one fluorescent colour to another (e.g., green to red) is concomitant with the againg of the protein and is useful for determination of the activation or deactivation of gene expression. The present sequence represents a non-fluorescent Discosoma sp. red fluorescent protein DsRed mutant, DsRed-NF, which has chromoprotein activity and which was generated in an example of the invention. The present sequence is not shown in the specification, but was derived from the wild-type DsRed sequence (ADH34489) shown in Fig 1 and the information provided on page Discosoma red fluorescent 25-MAR-2003 ABP56679; Sequence Synthetic Discosoma Discosoma; red ABPS6679 WPI; 2003-120798/11. 20-MAY-2002; 2002WO-US015968 28-NOV-2002 WO200294992-A2 Mammalian codon optimised Discosoma 18-MAY-2001; 2001US-0291871P (RIGE-) RIGEL PHARM INC 181 181 121 121 61 61 щ Н Similarity MRSSKNYIKEFMRFKVRMEGTVNGHBFBIEGBGBGRPYEGHNTVKLKVTKGGPLPFAWDI 225 LSPQFQYGSKYYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120 standard; YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225 KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180 LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI YMAKKPVOLPGYYYVDAKLDITSHNEDYTIVEQYERTEGRHHLFL KVKFIGVNFPSDGPVMQKKTMGWEACTERLYPRDGVLKGENHMALKLKDGGHYLVEFKSI Conservative Ş (first entry) fluorescent protein; protein; 98.3%; 98.2%; protein variant F125L 1; Score 1193; DF Pred. No. 2.4e-1; Mismatches red fluorescent protein; variant;
directed evolution; mutant. 4e-125 명 and Length Indels M183K. 225 0 Gaps 180 120 60

New Discosoma red fluorescent protein, useful for functional reporter for gene transcription, for target characterization localization of fusion proteins, or for scaffolds for protein

protein and

and

screens as a

Claim 8; Page; 22pp; English

libraries.

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RESULT 73
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                                                               18-MAY-2001; 2001US-0291871P.
                                                                                                                                                        28-NOV-2002
                                                                                                                                                                                                                                                                                                                   Discosoma;
                                                                                                                                                                                                                                                                                                                                        Mammalian
                                                                                                                                                                                                                                                                                                                                                                                     Discosoma
                     (RIGE-) RIGEL PHARM INC
                                                                                                            20-MAY-2002;
                                                                                                                                                                                                  WO200294992-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVKFIGVNFPSDGFVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
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                                                                                                                                                                                                                                                                                                                                        codon
                                                                                                                                                                                                                                                                                                                                                                                   red fluorescent protein variant F125V and
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                                                                                                              2002WO-US015968.
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                 n optimised Discosoma red fluorescent protein; variant; fluorescent protein; directed evolution; mutant.
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98.2%;
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Pred. No. 2.6e-125;
2; Mismatches 2;
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RESULT 74
AAE28837
ID AAE28
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AC AAE28
XZ
Z7-Di
DZ 27-Di
SX
Disco
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Fluol
KW Fluol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated Discosoma red fluorescent CC protein (I) comprising a 241 residue amino acid sequence (see ABP56678, CC S14, with one or more point mutations at amino acid position N24, F125, CC K164, or M183. Also described: (1) a fusion protein comprising the CC mucleic acid of (2); (4) a host cell comprising the vector; (5) a CC retroviral cDNA expression library comprising the vector; (5) a CC encoding (I); and (6) methods of making a fluorescent variant. The CC Discosoma red fluorescent proteins are useful for functional screens as a CC reporter for gene transcription (e.g. as a fusion protein), for target CC characterisation and localisation of fusion proteins, or for scaffolds (for protein and peptide libraries. The fluorescent proteins can also be CC used as selectable markers or reporter molecules for a variety of CC bioassays, including methods that use fluorescence activated cell sorting (PACS) as a selection mechanism. The method of directed protein evolution is useful for obtaining improved variants of red fluorescent protein. The CC variants of Discosoma red fluorescent protein have greatly improved CC is useful for blacosoma red fluorescent protein as compared to wild type or a codon optimised variant. The present sequence represents a mammalian CC codon optimised variant. The present sequence is not given in the CC specification, but is derived from the protein in Fig 1 as stated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                   AAE28837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-120798/11.
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                                                                                                                                                                                                                                                                                                                                                     YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRSSKNVI KEFMRFKVRMEGTVNGHEFEI EGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                               YKAKKPVQLPGYYYVDSKLDITSHHEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 121
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                                                                                                                                                                                                                                 protein;
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Pred. No. 3.4e-125;
2; Mismatches 2;
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Pluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay;

detector;

Discosoma sp.

drFP583 (NFP-6) mutant protein,

E5-NA.

mutant

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Best Local S
Matches 220
                                                                                                                                                                                                                                                                     The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drrP583 (NFP-6) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drrP583 (NFP-6) wild-type protein shown as SEQ ID NO:8 (AAEZ8833) in page 70-71 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Chidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2001; 2001US-0270983P.
04-DEC-2001; 2001US-00006922.
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Synthetic
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                                                                                                                                                                                                                                                 Sequence 225 AA;
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                                                                                                                                                               1 MRSSKOVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                          Similarity
                                                                                                 LSPQPQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
YMAKKPYQLPGYYYYDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                             KVKPIGVNPPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                LSPOFQYGSKYYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVATVTQDSSLQDGCFIY
                                                                                                                                      MASSENVITEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                            KVKF1GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE1HKALKLKDGGHYLVEFKS1
                                                                                                                                                                                            Conservative
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105
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Pred. No. 4e-1
2; Mismatches
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4e-125;
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                                                                                                                                                                                                                     Length 225;
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                                                                                   120
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AAE17542 standard; protein; 225
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181 YMAKKPVQLPGYYYVDTKLDITSHNEDYTIVEQYERTEGRHHLFL 225

RESULT 75 AAE17542 ID AAE1 Discosoma sp. AAE17542; (first entry) non-aggregating mutant timer protein ESNA

Fluorescent timer protein; protein movement; translocation; trafficking; promoter activity; gene expression; transgenic plant; gene modification; protein age; mutant; ESNA; mutein.

Synthetic **Discosoma** вр

WO200196373-A2 Misc-difference Misc-difference Misc-difference Location/Qualifiers /note= "Wild type Lys substituted with Thr" note= "Wild type Lys substituted with Glu" note= "Wild type Arg substituted with

20-DEC-2001

13-JUN-2001; 2001WO-US019097.

14-JUN-2000; (CLON-) CLONTECH LAB INC. 2000US-0211607P.

Fradkov AF, Terskikh

N-PSDB; 2002-154595/20.

New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, unfor monitoring intracellular protein movement, translocation, traff trafficking

Claim 5; Fig 3; 89pp; English.

CC The invention relates to a fluorescent timer protein having an emission CC spectrum that changes over time after synthesis from a first wavelength CC to a second wavelength. The fluorescent timer proteins are useful in CC monitoring the activity of a promoter, determining the age of a protein, CC enriching an agent that modulates the activity of a promoter and in CC enriching a population of cells comprising a fluorescent timer protein. CC The fluorescent timer proteins are also useful for assessing gene CC expression during development of a multicallular organism or during CC cellular differentiation, in response to a drug or other inducer of CC promoter activity, as a reporter to serve as a read-out of promoter CC activity, monitoring intracellular protein movement or translocation, CC protein trafficking, or protein stability, to investigate temporal CC aspects of the activity of a regulatory element, for determining cell crimiting development and organ remodelling, in spatial and temporal CC visualisation of newly synthesised proteins and accumulated proteins, and CC visualisation and extracellular matrix components. The fluorescent cumer proteins may further be used to investigations where photobleaching CC techniques are employed, as detectable labels, as selectable markers, as CC biosensors in prokaryotic and eukaryotic cells, in protease cleavage as assays, and as second messenger detectors. The nucleic acids can be used CC modifications in cell lines. The present sequence is Discosoma sp. ESNA

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RESULT 76
ABP56682
ID ABP56
XX ABP56
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The present invention describes an isolated Discosoma red fluorescent protein (1) comprising a 241 residue amino acid sequence (see ABP56678, S1), with one or more point mutations at amino acid position N24, F125, K164, or M183. Also described: (1) a fusion protein comprising (1); (2) an isolated nucleic acid encoding (1); (3) a vector comprising the nucleic acid of (2); (4) a host cell comprising the vector; (5) a retroviral cDNA expression library comprising the nucleic acid of (2), where the comprising the vector comprising the vector.
                                                                                                                                                                                                                                                                                                                              New Discosoma red fluorescent protein, useful for functional screens as reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptid
                                                                                                                                                                                                                                                 Claim 13; Page; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIGE-) RIGEL PHARM
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                                                                                                                                                                                                                                                                    Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; blosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; emmacreen: second messenger detector; drFP583 protein; NFP-6; mutein;
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Matches 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Chidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
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04-DEC-2001; 2001US-00006922.
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                                                                          Red fluorescent protein variant (DsRed)
                                                                                                                                                                         ADH10227 standard; protein;
                                              Protein immobilisation; red fluorescent protein; DsRed
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Matches 219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a carrier comprising a protein immobilized adsorptively, where the protein has a sulfhydryl group. The carrier useful for immobilizing polypeptides via the carboxyl group of the C terminus. The present sequence represents a Red fluorescent protein variant (DsRed) sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New carrier, useful for immobilizing polypeptides via the carboxyl g of the C-terminus, comprises a protein immobilized adsorptively, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 7; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  naving a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-045224/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2003; 2003EP-00253252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1367121-A2
                                                                                                                       Unidentified
                                                                                                                                                                                                           13-JAN-2005
                                                                                                                                                                                                                                                           ADT77526 standard; protein; 225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NAAD-) NAT INST ADVANCED IND
                                                                                                                                             target
                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                     ADT77526;
                                              09-APR-2004; 2004WO-JP005150
                                                                       21-OCT-2004
                                                                                               WO2004090542-A1
                                                                                                                                                          Protein array; planar substrate; immobilisation;
(NAAD-) NAT INST ADVANCED IND
                      10-APR-2003; 2003JP-00106450
                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                               substance.
                                                                                                                                                                                   SEQ ID NO: 2 used in protein array
                                                                                                                                                                                                                                                                                                                                                                                                                                           LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                         KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sulfhydryl group.
                                                                                                                                                                                                                                                                                                                          YMAKKPYQLPGYYYVDAKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                       YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                          KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGETHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                           LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVATVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASSENVITEFWRPKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirota K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                            (first
                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.7%;
97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1186; DB 8;
Pred. No. 1.5e-124;
2; Mismatches 4;
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SCI & TECHNOLOGY
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RESULT 80
ADH10228
ID ADH10
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AC ADH1(
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DT 11-MJ
XX
DE Immo
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Prot
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DS Synt
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PS S91:
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PD 03-
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PF 23-
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino groups of the polymer compound on the substrate. The invention further relates to a method for the preparation of the protein array. Preferably, the planar substrate has water absorptivity, the polymer used is a polyallyl amine or a polylysine, and the immobilised proteins contain a linker peptide. The protein array of the invention enables the effective and highly sensitive detection of various target substances. Sequences ADT77525-ADT77526 represent proteins whose C-termini were joined to a negatively charged acidic linker peptide (ADT77529) to produce the sequences shown in ADT77527-ADT77528. Sequences ADT77527-ADT77528 were subsequently immobilised on a planar substrate via the
                                  23-MAY-2002;
                                                                                                  03-DEC-2003
                                                                                                                                EP1367121-A2
                                                                                                                                                                                               Protein immobilisation; red
                                                                                                                                                                                                                           Immobilised red fluorescent
                                                                                                                                                                                                                                                            11-MAR-2004
                                                                                                                                                                                                                                                                                                                        ADH10228 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a substrate for a protein array, obtained by combining a polymer compound having primary amino groups in repeating units on a surface of a planar substrate. The invention also relates to a protein array formed by bonding the C-termini of proteins to the primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Substrate for protein array, having primary amino groups
    (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY
                                                                 23-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 225
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                                                                                                                                                                                                                                                                                                                                                                                                                           YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPQFQYGSKVYVXHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGETHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVATVTQDSSLQDGCFIY
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                                                                                                                                                                                                                                                                                                                                                                                                      YMAKKPVQLPGYYYVDAKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                  2002JP-00148950
                                                                 2003EP-00253252.
                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form a protein array.
                                                                                                                                                                                                                                                                                                                        protein;
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97.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; 32pp; Japanese.
                                                                                                                                                                                             fluorescent protein; DsRed.
                                                                                                                                                                                                                                                                                                                          239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1186; DB 8;
Pred. No. 1.5e-124;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ά
                                                                                                                                                                                                                            protein variant (DsRed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtained by combining a polymer compound in repeating units on surface of planar
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RESULT 81
ADT77528
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a carrier comprising a protein immobilized adsorptively, where the protein has a sulfhydryl group. The carrier is useful for immobilizing polypeptides via the carboxyl group of the Cterminus. The present sequence represents an immobilised red fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 239 AA;
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                                                                            10-APR-2003; 2003JP-00106450.
                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein/linker peptide SEQ ID NO:4 used in protein array.
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                           (NAAD-) NAT
                                                                                                                                09-APR-2004; 2004WO-JP005150
                                                                                                                                                                                    21-OCT-2004.
                                                                                                                                                                                                                                        WO2004090542-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein array;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein variant (DsRed) sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YMAKKPVQLPGYYYVDAKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     planar substrate; immobilisation;
ce; linker peptide.
                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                          226. .239
                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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97.3%;
                                                                                                                                                                                                                                                                                      "Corresponds to the linker peptide shown the specification"
                                                                                                                                                                                                                                                                                                                                                                      "Corresponds to
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Pred. No. 1.6e-124;
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                           & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                        NO:2"
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RESULT 82
ABP56686
ID ABP56
XX ABP56
XX 25-MA
XX 25-MA
XX DE D1sco
XX Mamma
KW D1scc
CX D1scc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a substrate for a protein array, obtained by combining a polymer compound having primary amino groups in repeating units on a surface of a planar substrate. The invention also relates to a protein array formed by bonding the C-termini of proteins to the primary amino groups of the polymer compound on the substrate. The invention further relates to a method for the preparation of the protein array. Preferably, the planar substrate has water absorptivity, the polymer used is a polyallyl amine or a polylysine, and the immobilised proteins contain a linker peptide. The protein array of the invention enables the effective and highly sensitive detection of various target substances. Sequences ADT77527-ADT7528 represent proteins comprising a C-terminal negatively charged acidic linker peptide (ADT77529) which were immobilised on a planar substrate via the linker peptide to form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substrate for protein array, obtained by combining a polymer compound having primary amino groups in repeating units on surface of planar substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-766496/75
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                                                                                                                                                                                                                                                                            Discosoma
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Discosoma red fluorescent protein variant R18H,N24S,F125L and M183K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP56686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP56686 etandard;
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                                                                                                                                                                                                                                                                                                                                                            Discosoma;
                                                                                                                                                                                                                                                                                                                                                                                   Mammalian
                                                                                                                                                                                                                         WO200294992-A2
                                                         18-MAY-2001; 2001US-0291871P
                                                                                                               20-MAY-2002; 2002WO-US015968.
                                                                                                                                                                     28-NOV-2002
     (RIGE-)
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        RIGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPQFQYGSKYYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVATVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVKFIGVNFPSDGFVMQKKTMGWEASTERLYFRDGVLKGETHKALKLKDGGHYLVBFKSI
                                                                                                                                                                                                                                                                                                                                                         codon optimised Discosoma red fluorescent protein; variant; red fluorescent protein; directed evolution; mutant.
                                                                                                                                                                                                                                                                                                      gp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
        PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.7%;
97.3%;
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Pred. No. 1.6e-124;
2; Mismatches 4;
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SXEXEXEXEX

ADL26532;

20-MAY-2004

(first entry)

ADL26532 standard;

protein;

226

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Discosoma fluorescent protein dsFP583.

Discosoma sp

fluorescent protein; fluorescent marker; gene expression; protein localization;  ${\tt FP}$ .

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RESULT 83
ADL26532
ID ADL26
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Discosoma red fluorescent protein, useful for functional screens as a reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-120798/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 240 AA;
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                                                                                                      182
                                                                                                                                            181
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                                                                                                                                                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                     VRSSKNVIKEFMRFKVHMEGTVSGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                             MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHVTVKLKVTKGGPLFFAWDI
                                                                                                                                      YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                      YKAKKPVQLPGYYYVDSKLDITSHHEDYTIVEQYERTEGRHHLFL 226
                                                                                                                                                                                     KVKLIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.4%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1183; DB 6; Pred. No. 3.5e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 240;
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RESULT 84
ADC24129
ID ADC24
XX
AC ADC24
XX
DT 18-DE
XX
Discc
XX
Discc
XX
Fluoi
KW Fluoi
KW Fluoi
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                       Discosoma red fluorescent protein; DsRed; AB interface; AC inte fluorescent protein variant; transcription induction detection;
     27-MAR-2003
                                                          US2003059835-A1
                                                                                                                                             Synthetic.
                                                                                                                                                                                               fluorescent protein variant; transcription induction detectio fluorescence energy resonance transfer; FRET; protein kinase; protein phosphatase; ion indicator; mutant; mutein; fast Tl.
                                                                                                                                                                                                                                                                                                                                               Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC24129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC24129 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides protein and coding sequences of novel fluorescent proteins. These are useful in pharmaceutical compositions and as fluorescent markers for gene expression and protein localization in cellular, developmental or molecular biology, particularly for measuring time-dependent cellular process such as protein diffusion and transport, also for optical information storage. The present sequence is a Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New
and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMAXA GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKST 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRBSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHMTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                                                                                                                               red
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                         fluorescent protein variant fast
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97.8%;
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Pred. No. 2.2e-123;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001US-00794308
24-MAY-2001; 2001US-00866538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 4; 67pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-2002; 2002US-00121258
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181
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216; Conserv
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                                                                                                                                                                                                                                                                             MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDI
YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERAEGRHHLFL
                         YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                 KVKF1GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE1HKALKLKDGGHYLVEFKS1
                                                                                                         KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                             LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGSFIY
                                                                                                                                                                                      LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                             MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                                                                                                                            95.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                         Score 1160; DB 7;
Pred. No. 1.2e-121;
3; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                 Length 225;
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RESULT 85
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Best Local Similarity
Matches 216; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    red fluorescent protein; DsRed; fluorescence; red wavelength; oligomerization; tetramerization; immunoassay; hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 4; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           movement in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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29-JUL-2002;
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                                                                                                                                                                                                                                                                                                          Sequence 225 AA;
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                                                                                                                                                                                                                                                                                                                                       T1 protein.
                                                                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                         LSPQFQYGSKYYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                       KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                   WASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
                YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
YMAKKPVOLPGYYYVDSKLDITSHNEDYTIVEQYERAEGRHHLFL 225
                                                           KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                       LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMVFEDGGVVTVTQDSSLQDGSFIY
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                                                                                                                                                                                                                                                Conservative
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2002US-00209208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fluorescent protein (DsRed) variant T1 protein.
                                                                                                                                                                                                                                                           95.6%;
96.0%;
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                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                              Score 1160;
Pred. No. 1.
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                                                                                                                                                                                                                                                                               DB 7; Length 225;
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RESULT 86
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Matches 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Discosoma red fluorescent protein (DsRed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 24; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    movement in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-845265/78.
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29-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligomerization;
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                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                       215;
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                                                                                                                                                                                        1 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRFYEGHVTVKLKVTKGGFLFFAWDI
                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNPEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                      MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                   KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                          LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGSFIY
                                                  KVKFRGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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2002US-00209208.
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                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                     95.0%;
95.6%;
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Pred. No. 7.6e-121;
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                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                    Length 225;
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181 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERAEGRHHLFL 225

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CC at least 80% identity to the GPP superfolding mutant appearing as CC ADMI3535 that has at least one amino acid substitution selected from CC e.g., a substitution at position 30 that is an arginine or a conservative CC variant of arginine and measurable fluorescence activity. Also included CC are directed-evolution for generating an enhanced folding variant of a CC target polypeptide (comprising mutating a polymucleotide encoding CC linking mutated polymucleotides, CI inking mutated polymucleotides to polypeptide encoding folding cC interference domain to form fusion protein (FP) constructs, expressing CC interference domain to form fusion protein (FP) constructs, expressing CC interference domain to form fusion protein (FP) constructs, expressing CC interference domain to form fusion protein generated by the method, an comparison of a fluorescent protein generated by the method, an comparison for a fluorescent protein generated by the method, an command of a fluorescent protein generated by the method, an comparison protein, mutating the first domain of the polypeptide to a poorly folding of command the poorly folding of protein comprising multiple domains comprotein in comparison protein, mutating the second domain, thus identifying a first domain with enhanced folding, joining a second domain, thus identifying a comprision to a fusion protein to form a second fusion protein, mutating the second domain, and detecting an increase in the comparison to a fusion protein to form a second fusion protein in comparison to a fusion protein to form a second fusion protein in comparison to a fusion protein mutated fusion protein in comparison to a fusion protein and detecting an increase in the comparison to a fusion protein, and detecting an increase in the comparison to a fusion protein, and detecting an increase in the comparison to a fusion protein, and detecting an increase in the comparison protein in soluted mucleic acid encoding the GPP, an expression vector comprising the mucleic acid called comparison to a f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a green fluorescent protein (GFP) that comprises at least 80% identity to the GFP superfolding mutant appearing as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; SEQ ID NO 41; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified green fluorescent protein, useful expression studies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFP; superfolder mutant; mutein; directed-evolution; folding inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfolding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2003; 2003US-00423688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WALD/) WALDO G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cant; mutein; green fluorescent protein;
folding interference domain; reporter protein;
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RESULT 8
ADC24131
ID ADC24131

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Best Local
                                                                                                                                   Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting transcriptional activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enhanced folding variant of target polypeptide and for improving folding and solubility of a target protein. The present sequence represents a coral DsRed enhanced folding variant. NOTE: The authors refer to SEQ ID 38-42 as SEQ ID 1-5 throughout the specification and never refer to SEQ ID 1-37 by number, it is obvious that SEQ ID 38-42 are meant to be SEQ II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001US-00794308.
24-MAY-2001; 2001US-00866538.
                                                                                                                                                                                                                                                       N-PSDB; ADC24130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fluorescent protein variant; transcription induction detection; fluorescence energy resonance transfer; FRET; protein kinase; protein phosphatase; ion indicator; mutant; dimer2; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Discosoma red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003
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                                                                                 Claim 12; SEQ ID NO 6; 67pp; English
                                                                                                                                                                                                                                                                               WPI; 2003-743764/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2002; 2002US-00121258
                                                                                                                                                                                                                                                                                                                                                                                             CAMP/) CAMPBELL R
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                                                                                                                                                                                                                                                                                                                                         RY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                                                                                                                      Campbell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fluorescent protein variant dimer2
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92.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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1.8e-118;
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The invention Discosoma red

describes a polynucleotide (fluorescent protein (DsRed)

sequence (I) encoding a
variant having a reduced

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC protein fluorescence, and assaying fluorescence of the variant CC fluorescent protein produced by (VII), where variant fluorescent protein protein a fluorescence of the variant fluorescent protein CC fluorescent protein is indicative of transcriptional activity. A polymucleotide ce encoding a fusion protein is useful for the analysis of in vivo CC localisation or trafficking of a polypeptide of interest. A polypeptide carrier is useful as markers to identify the location and amount of a CC target protein produced, where the target protein is fused to the marker, CC as a complement to or alternative for the green fluorescent protein or CC its spectral variant, for detecting induction of transcriptions, in CC which detects events as the function of the movement of fluorescent general contains and molecules such as Ca2+, Zn2+, for identifying the CC presence of a molecule in a sample, for identifying a specific CC presence of a molecule in a sample, for identifying a specific CC useful for identifying a region or condition that regulates the activity CC of an expression control sequence. This is the amino acid sequence of CC Discosoma red fluorescent protein variant dimer2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               propensity to oligomerise, comprising amino acid substitutions at the AB and/or AC interfaces of the wild-type DsRed sequence (S1) comprising 225 amino acids, given in the specification, where the substitutions result in reduced propensity of the DsRed variant to form tetramers. (I) is useful for detecting transcriptional activity by providing a host cells conatining a vector which comprises (I) operatively linked to an expression control sequence, and an unit to assay the variant fluorescent
                                                                                                                                                                                    red fluorescent protein; DsRed; fluorescence; red wavelength; oligomerization; tetramerization; immunoassay; hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 226
                                                                                                                                                                                                                                              Discosoma
                                                                                                                                                                                                                                                                                 20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                             ADL46208 standard; protein; 226
10-APR-2002; 2002US-00121258
                                   09-APR-2003; 2003WO-US010879
                                                                                                             WO2003086446-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYM
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                                                                                                                                                                                                                                          red fluorescent protein (DsRed) variant dimer2 protein.
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                                                                                                                                                                                                                                                                                 (first entry)
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Pred. No. 3.1e-117;
7; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the BRED polynomerical to form tetramers and where the variant displays detectable pasted variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed variant dimer2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful in molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 6; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                           Humanised anthozoa novel fluorescent protein hybrid drFP583/dmFP592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY99838 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   movement in cells.
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                                                                                                                                                                                           Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2000
                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                   Anthozoa; drFP583; fluorescent protein; non-bioluminescent organism;
                                                                                           WO200034326-A1.
                                                                                                                                                                                                                                                   fluorescent labeling; hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQFQYGSKAYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGTLIYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POFQYGSKVYVKHPADIFDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKKPYQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKKPVQLPGYYYVDTKLDITSHNEDYTIVEQYERSEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFRGTNFPPDGPVMQKKTMGWEASTERLYPRDGVLKGEIHQALKLKDGGHYLVEFKTIYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1121; Di
Pred. No. 3.1e
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; DB 7;
3.1e-117;
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15-JUN-2000

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RESULT 91
AAE28835
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XX AAE28
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DT 27-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coding region fragments from drFPS83 and dmFPS92 were digested with CC restriction endonucleases and combined together to produce a hybrid CC construct. drFPS83 is a full-length cDNA encoding a novel fluorescent CC protein (nFP) from Discosoma sp. "red", a non-bioluminescent species of the Class Anthozoa. The hybrid sequence was changed to optimise the CC codons for expression of the protein in mammalian cells. Fluorescent CC proteins can be used in fluorescent labeling, a useful tool for marking a CC protein, cell or organism of interest. Unlike other markers used in CC protein, do not require an exogenous cofactor or substrate. Methods CC involving fluorescent proteins are also less laborious and less difficult CC control than the traditional methods of fluorescent labeling, where a CC fluorophore derivative. Novel fluorescent proteins isolated from species of the Class Anthozoa can be used as markers for gene expression and CC protein localization studies, and in fluorescence resonance energy CC transfer (FRET) reactions. They may have improved properties and better cuitability for larger excitations compared to prior art fluorescent CC suitability for larger excitations compared to prior art fluorescent contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 206
                                   Discosoma sp. drFP583/dmFP592 (6/9Q) protein
                                                                        27-DEC-2002
   Fluorescent protein; chromoprotein; protease cleavage assay; filter;
                                                                                                           AAE28835
                                                                                                                                               AAE28835 standard;
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14-OCT-1999;
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)B; AAA48748.
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                                                                                                                                                                                                                                                            YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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99US-00418529.
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                                                                                                                                             protein;
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91.6%;
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Pred. No. 5.1e-117;
12; Mismatches 7;
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RESULT 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583/dmFP592 (6/9Q) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Chidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fluorescence activated cell sorting application; fluorescent timer; blosensor; fluorescence resonance energy transfer application; PRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; dmFP592 protein.
                                              19-SEP-2000 (first entry)
                                                                                                              AAY99839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 225 AA;
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04-DEC-2001; 2001US-00006922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                              standard; protein; 225
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                                                                                                                                                                                                                                                                                                                                              LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1119; DB 5;
; Pred. No. 5.1e-117;
12; Mismatches 7;
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Humanised Anthozoa novel fluorescent

protein

hybrid drFP583/dmFP592-2G

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CC novel fluorescence proteins isolated from species of the Class Anthozoa CC and be used as markers for gene expression and protein localization.

CC proteins and the covalent are fluorescence protein localization.

CC proteins and help less difficult proteins su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 79; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel fluorescent protein from non-bioluminescent Discosoma useful for fluorescent labeling and as markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lukyanoy SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-1998;
14-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anthozoa; drPP583; fluorescent protein; non-bioluminescent organism; fluorescent labeling; hybrid; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 225 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             fluorescent protein
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                          KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                      LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                              LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY
                                                                                                                                                                                                                                                 MSCSKNVIKEFMRFQVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI
                                                                                                                                                                                                                                                                        MRSSKAVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                labeling;
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fradkov AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00210330
99US-00418529
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                                                                                                                                                                                                                                                                                                                                 91.5%; Score 1111; DB 3;
90.7%; Pred. No. 4.1e-116;
tive 14; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labas YA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green
                                                                                                                                                                                                                                                                                                                                                                        Length 225;
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Best Local S
Matches 204
                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening, as subsensors in prokaryotic and eukaryotic cells, in screening, as biosensors in prokase cleavage assays or as fluorescence timers. The present in protease cleavage assays or as fluorescent timers. The present in gequence is Discosoma sp. drFP583/dmFP592 (6/90) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drFP583/dmFP592 (6/90) wild-type protein shown as SEQ ID NO:12 (AAE28835) in page 72-73 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; dmFP592 protein
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a non-aggregating chromo- or fluoresco
of an aggregating Chidarian chromo- or fluorescent protein or me
analyte detection assays or fluorescence activated cell sorting
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                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lukyanov S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2001;
04-DEC-2001;
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                                                                                                                                                                                                                                        204;
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                                                                                                                                                                                                                                                                       Similarity
LSPOPOYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLODGCFIX 120
                                                                                                                                                                                                                                                                                                                                                              225 AA;
                                                                                                                        MSCSKNVIKEFMRFQVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI
                                                                                                                                                 MRSSKNVIKBEMREKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                           Conservative
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2001US-00006922
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217
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                                                                                                                                                                                                                                                                       91.5%;
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                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                           Score 1111; DB 5;
Pred. No. 4.1e-116;
4; Mismatches 7;
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protein or mutant for
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                                                            The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in protearyotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583/dmFP592 (6/9Q) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drFP583/dmFP592 (6/9Q) wild-type protein shown as SEQ ID NO:12 (AAE28835) in page 72-73 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Chidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
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04-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sunscreen; second messenger detector; drFP583 protein; dmFP592 protein;
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2001US-00006922
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The present sequence is derived from humanised hybrid protein CC drep583/dmFP592. drFP583 is a full-length cDNA encoding a novel CC drep583/dmFP592. drFP583 is a full-length cDNA encoding a novel CC fluorescent protein (nFP) from Discosoma sp. "red", a non-bioluminescent Species of the Class Anthozoa. The hybrid sequence was changed to Optimise the codons for expression of the protein in mammalian cells. The CC which were incorporated by random mutagenesis. Fluorescent proteins can CC be used in fluorescent labeling, a useful tool for marking a protein, CC cell or organism of interest. Unlike other markers used in proteins CC labeling, such as beta-galactosidase and luciferase, fluorescent proteins CC do not require an exogenous cofactor or substrate. Methods involving CC fluorescent proteins are also less laborious and less difficult to control than the traditional methods of fluorescent labeling, where a CC protein of interest is purified and then covalently conjugated to a
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; dmFP592 protein
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Misc-difference 83
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                                                                              Lukyanov S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gp.
                                                                              Lukyanov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drFP583/dmFP592 (6/9Q) mutant protein (K15Q+K83M+T217S)
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Lys substituted 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Wild-type Thr substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.0%;
                                                                                ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Wild-type Lys substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 1105; DB 3;
; Pred. No. 1.9e-115;
14; Mismatches 8;
                                                                                Yanushevich
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                                                                                   Υ,
                                                                                Savistky A,
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP593/dmFP592 (6/90) mutant protein of the invention. Note: This sequence is not shown in the specification, but is derived from Discosoma sp. drFP593/dmFP592 (6/90) wild-type protein shown as SEQ ID NO:12 (AAE28835) in page 72-73 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Chidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
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applications.
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WPI; 2000-423379/36.
N-PSDB; AAA28958.
                                                                                                                                                                                                                                                                                                         Discosoma sp.
                                                                                                                                                                                                                                                                                                                                                                 AAY92894;
                                                                                                                                                                                                                                                                                                                                                                                             AAY92894
                                                                                                                                                                                                      WO200034324-A1
                                                                                                                                                                                                                                                                             dmFP592; fluorescent protein; non-bioluminescent; label; marker;
                                                                                                                                                                                                                                                                                                                                       12-SEP-2000
                                                                                                    11-DEC-1998;
19-NOV-1999;
                                                                                                                                                                           15-JUN-2000
                                                                                                                                                                                                                                                              fluorescence resonance energy transfer reaction; FRET
                                                                                                                                              10-DEC-1999;
                                                                       (CLON-) CLONTECH LAB INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSPQFQYGSKYYYKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVKFIGVNFPSDGPVMQRRTRGWEASSERLYPRDGVLKGDIHMALRLEGGGHYLVEFKSI
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                                           SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERSEGRHHLFL
                                                                                                                                                                                                                                 gp.
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                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                         "magenta" fluorescent protein dmFP592
                                                                                                    98US-00210330.
99US-00444341.
                                                                                                                                               99WO-US029412
                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.0%;
90.2%;
                                              ΑF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                              Labas
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Pred. No. 1
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                                              YA,
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                                              Matz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is a novel fluorescent protein (dmPP592) from Discosoma sp.

"magenta", a non-bioluminescent species of the genera Anthozoa. The
fluorescent colour is observed under usual white light or ultraviolet
light. It has an absorbance maximum at 573 nm and an emmision maximum at
593 nm. The polynucleotides of the invention can be used to produce the
proteins recombinantly, and as a source of primers and probes for
identifying related proteins. The fluorescent proteins have applications
in fluorescent labeling, as fluorescent markers for gene expression and
protein localization studies, and in fluorescence resonance energy
transfer (FRET) reactions. They may have improved properties and better
suitability for larger excitations, compared to prior art fluorescent
proteins such as green fluorescent protein from Aequorea victoria, which
has an excitation maximum at 395 nm, a second excitation peak at 475 nm
c and an emission maximum at 510 nm
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Best Local
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                                                                                                                                        10-DEC-1999;
                                                                                                                                                                        15-JUN-2000.
                                                                                                                                                                                                                                       Discosoma
                                                                                                                                                                                                                                                                   Anthozoa; fluorescent protein; fluorescence labeling; amFP486; cFP484; zFP506; zFP538; drFP583; dsFP483; asFP600; dgFP512; dmFP592.
                                                                                                                                                                                                                                                                                                                 Discosoma sp. magenta fluorescent protein dmFP592.
             WPI; 2000-423451/36
                                            Lukyanoy SA,
                                                                                                          11-DEC-1998;
                                                                                                                                                                                                        WO200034526-A1
                                                                                                                                                                                                                                                                                                                                                 12-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                               AAB01625;
                                                                                                                                                                                                                                                                                                                                                                                                           AAB01625 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel fluorescent protein from non-bioluminescent Discosoma species, useful for fluorescent labeling and as markers.
                                                                           (CLON-)
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                                                                           CLONTECH LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YMAKKP-VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                                             Fradkov
                                                                                                          98US-00210330
                                                                                                                                         99WO-US029405
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                                                                                                                                                                                                                                                                                                                                                entry)
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                                             AF,
                                             Labas
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                                            YA,
                                             Matz
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ARESULT 99
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                         14-OCT-1999;
15-OCT-1999;
15-OCT-1999;
19-NOV-1999;
19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anthozoa; Chromoprotein; fluorescent protein; dmFP592; NFP-9; sunscreen; analyte detection assay; selectable marker; recombinant DNA application;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2003
19-JUN-2001
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                                                                                                                                                                                                              13-OCT-2000;
                                                                                                                                                                                                                                                                          19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                        Discosoma sp; magenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Discosoma
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                                                                                                                                                                                                                                                                                                                                  WO200127150-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      biosensor; pH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 71-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YMVKKPSVQLPGYYYVDSKLDMTSHNEDYTVVEQYEKTQGRHHPFI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMAKKP-VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPOPOYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSPOFOYGSKVYVKHPADIPDYKKLSFPEGFKWERVMVFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSCSKNVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp. magenta chromo/fluorescent protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                              2000WO-US028477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      indicator;
                     99US-00418529.
99US-00418917.
99US-00418922.
99US-00444338.
99US-00444341.
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88.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          invivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dmFP592 (NFP-9).
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RESULT 100
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Best Local Simi
Matches 199;
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14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
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09-DEC-1999;
09-DEC-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a Discosoma sp. magenta chromo/fluorescent protein, dmFP592 (NFP-9). NFP-9 is present in an environment other than its natural environment and has an absorbance maximum ranging from 375nm to 775nm and more usually from 560nm to 590nm and emission maximum ranging from 395nm to 795nm and more usually from 580 to 610nm. The chromoproteins or fluorescent proteins are useful as labels in analyte detection assays, as selectable markers in recombinant DNA applications, as biosenseors in prokaryotic and eukaryotic cells e.g. as pH indicator and as in vivo markers in animals. They are also useful in sunscreens an as selective filters. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An Anthozoa chromo- or fluorescent protein (other than its natural environment, useful a detection assays and as a selectable marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2000;
14-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 230 AA;
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                                                                                                   ABP70038 standard;
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           Colour Facilitating molecule
                                     06-AUG-2003
22-JAN-2003
                                                                          ABP70038
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                     MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 9; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SA,
                                                                                                                                                                              YMAKKP-VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                       KVKFIGVNFPSDGPVMQKKTMGWBASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                                                   LSPOPQYGSKVYVKHPADIPDYKKLSPPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY
                                                                                                                                                                                                                                                                                                                      MSCSKNVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI
                                                                                                                                                                 YMVKKPSVQLPGYYYVDSKLDMTSHNEDYTVVEQYEKTQGRHHPFI 226
                                                                                                                                                                                                                   EVKFIGVNFPSDGPVMQRRTRGWEASSERLYPRDGVLKGDIHMALRLEGGGHYLVEFKSI
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2000US-0211609P.
2000US-0211627P.
2000US-0211687P.
2000US-021188P.
2000US-0211880P.
2000US-0211880P.
2000US-0211880P.
2000US-0211880P.
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(first en
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99US-00458144.
99US-00458477.
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                                                                                                   protein; 230
                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                     89.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Labas
                                                                                                                                                                                                                                                                                                                                                                                     Score 1085.5;
Pred. No. 3.16
           (CFM)
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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              related
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                                                                                                                                                                                                                                                                                                                                                                                     5; DB 4
3.1e-113;
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as a label in analyte
r in recombinant DNA
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             sequence
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or compressing a polypeptide which, in a cell, alone or together with one or compression coloured coloured singarts an altered visual characteristic to the cell coloured their molecules emission. CFMs are useful for producing a cc transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant cc extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional clight for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car cupholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, cc expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in cg situations of distorted light spectra (biomatrix). The first all-protein cc chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 199
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21-MAR-2001;
15-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones EL, Karan M,
Hoegh-Guldberg IO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002; 2002WO-GB000928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 19; Page 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-740765/80
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(UYQU ) UNIV QUEENSLAND
(JONE/) JONES E L.
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                          WRSSKNVIKEFWRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
KVKFIGVNFPSDGPVMQKXTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                              LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                          MSCSKNVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI
                                                                                                                                                                                                                                                                                    89.4%; ilarity 88.1%; Conservative 1
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2001AU-00003874.
2001US-0329816P.
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                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                Score 1085.5;
Pred. No. 3.16
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                      .1e-113;
                                                                                                                                                                                                                                                                                                                                                DB 5;
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                                                                                                                                                                                                                                                                                            Indels
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EVKFIGVNFPSDGPVMQRRTRGWEASSERLYPRDGVLKGDIHMALRLEGGGHYLVEFKSI

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RESULT 101
ABP96651
ID ABP96652
XX ABP96652
AC ABP966
XX Chrome
Chrome
KW Chrome
KW att si
KW platfc
XX W02002
XX WPI;
PF 30-MAI
XX Perkil
PF 21-MAI
XX WPI;
PF W0401
PF W0
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                                                                                                                                                                         The present invention describes a eukaryotic chromosome (I) comprising cone or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of call lambda-integrase. Also described: (1) a platform artificial chromosome catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for cartificial chromosome, preferably an ACes. (II) is useful for cartificial chromosome, preferably an ACes. (II) is useful for cartificial chromosome, preferably an ACes. (II) is useful for cartificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or carminated cartier system, microinjection, microcall fusion, electroporation, by a carrier system, microinjection, microcall fusion, electroporation, carrier system, microinjection, microcall fusion, electroporation, call, preferably a stem cell or an embryo. (II) comprises a heterologous call, preferably a stem cell or an embryo. (II) comprises a heterologous call cacid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention
      Matches
                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2001;
21-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Red fluorescent protein (DsRed)
                                                                                                                            Sequence 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 192-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002; 2002WO-US017452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200297059-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP96651,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP96651 standard; protein; 230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-140461/13.
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      199;
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            œΉ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMAKKP-VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perez C, L
Shellard J;
                                                                                                                                  Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0294758P
2002US-0366891P
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                                   89.4%;
88.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lindenbaum M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272pp;
   17; Mismatches
Score 1085.5; DB 6;
Pred. No. 3.1e-113;
L7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein SEQ ID NO:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Greene A,
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      Indels
                                                              Length
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                                                                 230;
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   μ,
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MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60

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                                                                                                                                        14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
                                                                                                          14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Anthozoa; Chromoprotein; fluorescent protein; drFP583; NFP-6; sunscreen; analyte detection assay; selectable marker; recombinant DNA application; biosensor; pH indicator; invivo marker; selective filter.
An Anthozoa chromo- or fluorescent protein (P1) present in an enother than its natural environment, useful as a label in analyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2003
19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE00375;
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                             WPI; 2001-266409/27
N-PSDB; AAD03615.
                                                                                                                                                                                                                                                                                       14-OCT-1999;
                                                                                                                                                                                                                                                                                                                              19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                       Discosoma sp;
                                                                                                                                                                                                                          09-DEC-1999;
                                                                                                                                                                                                                                     09-DEC-1999;
                                                                                                                                                                                                                                                                                                          13-OCT-2000; 2000WO-US028477
                                                                                                                                                                                                        09-DEC-1999;
                                                                                                                                                                                                                                               19-NOV-1999;
                                                                                                                                                                                                                                                          19-NOV-1999;
                                                                                                                                                                                                                                                                  15-OCT-1999;
                                                                                                                                                                                                                                                                           15-OCT-1999;
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                                                                               CLONTECH LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                           SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMAKKP-VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVKFIGVNFPSDGPVMQRRTRGWEASSERLYPRDGVLKGDIHMALRLEGGGHYLVBFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YMVKKPSVQLPGYYYVDSKLDMTSHNEDYTVVEQYEKTQGRHHPFI 226
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                                                                                                  99WO-US029405

2000US-0211607P

2000US-02116269P

2000US-0211627P

2000US-0211687P

2000US-0211887P

2000US-0211888P

2000US-0211888P

2000US-0211888P
                                                                                                                                                                                                                                                                                                                                                                                                                        red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  red chromo/fluorescent
                                                                                                                                                                                                                                              99US-00444341.
                                                                                                                                                                                                                                                                  99US-00418922.
                                                                                                                                                                                                        99US-00458477.
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    150. .151
/note= "Encoded by TIGTATCCTCGTGATGGCGTGTTGAAAGGAGAGATT
CATAAGGCTCTGAAGCTGAAAGACGGTGGT"
                                                                                                                                                                                                                                                         9US-00444338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                            ΑF,
                                                           Labas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205
                                                           YA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein,
                                                            Matz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drFP583
                                                            Terskikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NFP-6).
           environment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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RESULT 103
AAEDO384
ID AAEDO3
XX AAEDO3
XX AAEDO3
XX D1scoe
XX Anthoz
KW Anthoz
KW Anthoz
KW B10ser
XX B1scoe
OS Synthe
XX Ey
FH Key
FH Key
FH Key
FH Key
FH Misc-(
FT Misc-(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a Discosoma sp. red chromo/fluorescent protein, cc drpp583 (NFP-6). NFP-6 is present in an environment other than its cc natural environment and has an absorbance maximum ranging from 250nm to 750nm and more usually from 540nm to 580nm and enission maximum ranging cc from 275nm to 775nm and more usually from 565 to 605nm. The cromoproteins or fluorescent proteins are useful as labels in analyte cd detection assays, as selectable markers in recombinant DNA applications, cc as biosensors in prokaryotic and eukaryotic cells e.g. as pH indicator cc and as in vivo markers in animals. They are also useful in sunscreens and cc as elective filters. Note: The specification also refers to following cmutants of this sequence: (a) E5 with substitutions V105A and S197T, (b) E5down with substitution S197T, (c) E5T with substitutions V105A, I161, cc Substitutions V11M, V105A, V120H and S197T. However, the positions of S ci (updated on 11-8EP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                            Anthozoa; Chromoprotein; fluorescent protein; drFP583; NFP-6; sunscreen; analyte detection assay; selectable marker; recombinant DNA application; biosensor; pH indicator; invivo marker; selective filter; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 6; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                             Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE00384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE00384 standard;
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        14-OCT-1999;
                                                                                                                                                                          WO200127150-A2
                                                                                                                                                                                                                                                             Misc-difference
                                                             13-OCT-2000; 2000WO-US028477
                                                                                                                     19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRSSKNVIKEFMRFKVRMEGTVNGHEFBIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSSSLALNFPSDGPVMQKKTMGWEASTERL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВĎ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               red drfP583 (NFP-6) mutant E5up (V105A).
           9908-00418529
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                               /note= "Wild type Val substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%;
88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as a selectable marker in recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1058; DB 4;
Pred. No. 3.3e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205
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                                                                      RESULT 104
AAE00383
ID AAE003
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AAE00383;

AAE00383 standard; protein; 205

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Best Local Similarity
Matches 198; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1999;
15-OCT-1999;
19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                  The present sequence is a Discosoma sp. red chromo/fluorescent protein, drPp583 (NFP-6) mutant E5up (V105A). NFP-6 is present in an environment other than its natural environment and has an absorbance maximum ranging from 250nm and more usually from 540nm to 580nm and emission maximum ranging from 275nm to 775nm and more usually from 540nm to 580nm and emission fine chromoproteins or fluorescent proteins are usually from 565 to 605nm. The chromoproteins or fluorescent proteins are usually from 565 to 605nm. analyte detection assays, as selectable markers in recombinant DNA applications, as biosensors in prokaryotic and eukaryotic cells e.g. as pH indicator and as in vivo markers in animals. They are also useful in sunscreens and as selective filters. Note: The present sequence is not shown in the specification, but derived from drFP583 (NFP-6) sequence (AAE00375) shown in figure 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
14-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An Anthozoa chromo- or fluorescent protein (P1) present in an enother than its natural environment, useful as a label in analyte detection assays and as a selectable marker in recombinant DNA
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                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-266409/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-DEC-1999;
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161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA,
                                                                                                                     LSPQFQYGSKVYVKHPADIPDYKKLSPPEGFKWERVMNFEDGGVATVTQDSSLQDGCFIY
                                                                                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                       MRSSKNVIKBFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                            205 AA;
                   YMAKKPYQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                             KSSSLALNFPSDGPVMQKKTMGWEASTERL----
                                                                                   KVKFIGVNFPSDGFVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                   MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US029405.
2000US-0211607P.
2000US-0211626P.
2000US-0211627P.
2000US-0211687P.
2000US-0211766P.
2000US-0211766P.
2000US-0211766P.
2000US-0211880P.
2000US-0211880P.
                                                                                                                                                                                                                                               Conservative
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99US-00458477.
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99US-00457898.
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99US-00444338.
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                                                                                                                                                                                                                                                             86.8%;
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                                                                                                                                                                                                                                               Score 1054; DB 4;
Pred. No. 9.3e-110;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matz MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terskikh
                                                                                                                                                                                                                                                                             Length 205;
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                                                                                                                             120
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Query Match
Best Local S
Matches 198
                                                                             The present sequence is a Discosoma sp. red chromo/fluorescent protein, drFP583 (NFP-6) mutant E8 (N42H). NFP-6 is present in an environment other than its natural environment and has an absorbance maximum ranging from 250nm to 750nm and more usually from 540nm to 580nm and emission maximum ranging from 275nm to 775nm and more usually from 565 to 605nm. The chromoproteins or fluorescent presents are useful as labels in analyte detection assays, as selectable markers in recombinant DNA applications, as biosensors in prokaryotic and eukaryotic cells e.g. as bi midicator and as in vivo markers in animals. They are also useful in sunscreens and as selective filters. Note: The present sequence is not shown in the specification, but derived from drFP583 (NFP-6) sequence (AAE00375) shown in figure 6
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14-JUN-2000;
14-JUN-2000;
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09-DEC-1999;
09-DEC-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                      Sequence 205
                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                       An Anthozoa chromo- or fluorescent protein (P1) present in an environment other than its natural environment, useful as a label in analyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anthozoa; Chromoprotein; fluorescent protein; drPP583; NFP-6; sunscreen; analyte detection assay; selectable marker; recombinant DNA application; biosensor; pH indicator; invivo marker; selective filter; mutant; mutein
                                                                                                                                                                                                                                                                                                         detection assays and as a selectable marker in
                                                                                                                                                                                                                                                                                                                                                                                           Lukyanov SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2000;
14-JUN-2000;
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 y Match 86.7%;
Local Similarity 88.0%;
hes 198; Conservative
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2000US-0211609P
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2000US-0211626P
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                                                                                                                                                                                                                                                                                                                                                                                           Fradkov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9905-00458477.
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 Score 1053; DB 4;
Pred. No. 1.2e-109;
3; Mismatches 4;
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                           Length 205;
  Indels
  20;
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RESULT 105
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The invention describes a polynucleotide sequence (I) encoding a CC Discosoma red fluorescent protein (DsRed) variant having a reduced CC propensity to oligomerise, comprising amino acid substitutions at the AB CC and/or AC interfaces of the wild-type DsRed sequence (S1) comprising 225 CC amino acids, given in the specification, where the substitutions result in reduced propensity of the DsRed variant to form tetramers. (I) is CC useful for detecting transcriptional activity by providing a host cells CC conatining a vector which comprises (I) operatively linked to an CC expression control sequence, and an unit to assay the variant fluorescent protein fluorescence, and assaying fluorescence of the variant fluorescent protein produced by (VII), where variant fluorescent protein protein is useful for the analysis of in vivo localisation or trafficking of a polypeptide of interest. A polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Discosoma red fluorescent protein; DsRed; AB interface; AC interface; fluorescent protein variant; transcription induction detection; fluorescence energy resonance transfer; FRET; protein kinase; protein phosphatase; ion indicator; mutant; mRFPl; mutein.
                                                                                                                                                                                                                                                                                                          Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-743764/70.
N-PSDB; ADC24132.
                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 8; 67pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                              transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                               (TSIE/)
(CAMP/)
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24-MAY-2001; 2001US-00866538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSPOPOYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLODGCFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHHTVKLKVTKGGPLPFAWDI
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                                                                                                                                                                                                                                                             English.
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RESULT 106
ADL4621
ADL4622
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ADL4622
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ADT 20-MAY
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Best Local 8
Matches 192
                                                                                                                                                                                                                                                                                                                                     10-APR-2002; 2002US-00121258.
29-JUL-2002; 2002US-00209208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           red fluorescent protein; DsRed; fluorescence; red wavelength;
oligomerization; tetramerization; immunoassay; hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Discosoma red fluorescent protein (DsRed) variant mRFP1 protein
New monomeric and dimeric Anthozoan fluorescent protein variants reduced propensity to oligomerize, and encoding polynucleotides, in molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2003; 2003WO-US010879.
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                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                           2003-845265/78.
DB; ADL46211.
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Pred. No. 5.6e-106;
5; Mismatches 24;
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                            02-FEB-1998; 98US-00017412.
07-FEB-2000; 2000US-00499464.
24-MAY-2007; 2002US-00154758.
29-JAN-2003; 2003US-00353090.
09-APR-2003; 2003US-0461133P.
                                                                                                                                                                                                                                                     rluorescent protein; multi-colour PCA; drug discovery; target validation; high-throughput screening; high-content screening; pathway mapping; drug mechanism-of-action study; biosensor; diagnostic; red fluorescent protein; spectral shift: mprp1
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                                                                                                                                                                                                                                                                                                                            detectable signal; protein fragment complementation assay; interaction detection; biomolecular interaction detection;
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                                                                                                                                                                                                                                                                                                                                                                            fluorescent protein mRFP1.
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Pred. No. 5.6e-106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC protein fragment is fused to a separate molecule. Also described are: CC protein fragment complementation assays (PCAs) for detection of molecular interactions, involving reassembling separate fragments from an optically detectable protein, and detecting the reassembly by units of reconstitution of activity of the optically detectable protein, where the creassembly of the fragments is operated by the interaction of molecular commanism fused to each fragment, and is independent of other molecular compropriate optically detectable protein, effecting involving selecting an cappropriate optically detectable protein such that the fragmentation results in creversable loss of protein function, finsing or attaching fragments of the optically detectable protein separately to other molecules, reassociating the protein fragments through interactions of the molecules, reassociating companies, designing and engineering of PCAs based on fluorescent protein; and a method and composition for the construction of multi-color PCAs. (I) is useful in PCAs and other assays for drug discovery, target conspling, drug mechanism-of-action studies, biosensors and diagnostics. (CI) is useful for engineering different colour PCAs for applications in biology and biotechnology. This is the amino acid composition of applications in biology and biotechnology. This is the amino acid composition of isolated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition useful in protein fragment complementation assays for drug discovery and high-throughput screening, comprising complementary fragments of protein or mutant protein, generating optically detectable
                      25-AUG-2005
                                                               AEA54910;
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Pred. No. 5.6e-106;
5; Mismatches 24;
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N-PSDB; AEA54911.
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Araki T;
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27-JAN-2004; 2004JP-00018344
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                                               YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH
                                                                                                                                                            KVKLRGTNFPSDGPVMQKKTMGWEASTERMYPEDGALKGEIKMRLKLKDGGHYDAEVKTT 448
                                                                                                                                                                                                                        KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                 LSPOFQYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747 AA;
YMAKKPVQLPGAYKTDI KLDI TSHNEDYT I VEQYERAEGRH
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fusion protein; enhanced green fluorescent protein; EGFP;
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Pred. No. 3.
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Best Local Similarity
Matches 190; Conserv
                                                                                                                                                                                                                                                                                                                                                        The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the BBRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed variant mRFFP1.1 protein which contains a Q66M and a T147S mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   red fluorescent protein; DsRed; fluorescence; red wavelength; oligomerization; tetramerization; immunoassay; hybridization assay.
                                                                                                                                                                                                                                                                                                                             Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 70; SEQ ID NO 79; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful in molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-845265/78.
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29-JUL-2002; 2002US-00209208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Discosoma red fluorescent protein (DsRed) variant mRFP1.1 coding sequence
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               YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
                                                              KVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKMRLKLKDGGHYDAEVKTT 180
YMAKKPVOLPGAYKTDIKLDITSHNEDYTIVEQYERAEGRH 221
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Search completed: January 11, 2006, 02:08:28 Job time : 81 Becs

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No matches found
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Gapop 10.0 , Gapext 0.5
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1 MRSSKNVIKEFMRFKVRMEG......EDYTIVEQYERTEGRHHLFL 225
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Copyright (c) 1993 - 2006 Compugen Ltd.
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O1-FEB-2005 (Rel. 46, Created)
O1-FEB-2005 (Rel. 46, Last sequence update)
O1-FEB-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
- Fluorescent protein dreps83 (DsRed).
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                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=99436614, PubMed=10504696, DOI=10.1038/13657, MEDLINE=99436614, PubMed=10504696, DOI=10.1038/13657, Z
                                                                                                                                                                                                                                       Discosoma sp. (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
Discosomatidae; Discosoma.
   Matz M.V., Fradkov A.F., Labas Y.A., Savitsky
Markelov M.L., Lukyanov S.A.;
"Fluorescent proteins from nonbioluminescent
Nat. Biotechnol. 17:969-973(1999).
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                                          Anthozoa
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Q66nd8 discosoma s
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Q5s3g8 discosoma s
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                                       species.";
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Matches 225
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PubMed=11209050; DOI=10.1073/pnas.98.2.462;

Yarbrough D., Wachter R.M., Kallio K., Matz M.V., Remington S.J.;

Yarbrough D., Wachter R.M., Kallio K., Matz M.V., Remington S.J.;

President grotal structure of DsRed, a red fluorescent protein from coral, at 2.0-A resolution.";

Proc. Natl. Acad. Sci. U.S.A. 98:462-467(2001).

-- FUNCTION: Thought to play a role in photoprotection of the coral's resident symbiont microalgae's photosystems from photoinhibition caused by high light levels found near the surface of coral reefs. In deeper water, the fluorescence may be to convert blue light in the surface of coral reefs.
                                                                                                                                                                                                                                                                                                                                                                                          3D-structure;
MOD_RES 6
CROSSLNK 6
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PubMed=11101896; DOI=10.1038/81992;
Wall M.A., Socolich M., Ranganathan R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homolog DsRed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF168419; AAF03369.1; -; mRNA. PDB; 1G7K; X-ray; A/B/C/D=2-225. PDB; 1GGX; X-ray; A/B/C/D=1-225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Struct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               removed
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01353; GFP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requires nothing other than molecular oxygen.

BIOTECHNOLOGY: Fluorescent proteins have become a useful and ubiquitous tool for making chimeric proteins, where they function as a fluorescent protein tag. Typically they tolerate N- and C-terminal fusion to a broad variety of proteins. They have been expressed in most known cell types and are used as a noninvasive fluorescent marker in living cells and organisms. They enable a wide range of applications where they have functioned as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

SIMILARITY: Belongs to the GFP family.
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PTM: Contains a chromophore consisting of modified amino acid residues. The chromophore is formed by autocatalytic backbone residues. The chromophore is formed by autocatalytic backbone condensation between Xaa-N and Gly-(N+2), oxidation of Tyr-(N+to didehydrotyrosine, and formation of a double bond to the all amino nitrogen of residue Xaa-N. Maturation of the chromophore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the microalgal symbionts.
BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note=Exhibits a smaller absorbance peak at 494 nm. fluorescence emission spectrum peaks at 583 nm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abs (max) =558 nm;
                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            long as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                         Similarity
                                         LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY
                                                                                                                    MRSSKNVIKEFMRFKVRMEGTVNGHEFBIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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ĹŚPQFQYGŚKVYVKHPADIPDYKKLŚFPEGFKWERVMNFEDGGVVTVTQDŚŚLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR011584; GFP_related.
IPR000786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                 225 AA;
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                 756; Green_fl_protein; 1.
Chromophore; Luminescence; Photoprotein.
Chromophore; Luminescence; Photoprotein.
Chromophore; Luminescence; Photoprotein.
Chromophore; Luminescence; Photoprotein.
Chromophore; Luminescence; Photoprotein.
Chromophore; Photoprotein.
Chr
                                                                                                                                                                                                                                                                      100.0%; Score 1214; DB 1; 100.0%; Pred. No. 1e-96;
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                                                                                                                                                                                                                                                Mismatches
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"Cloning of Anthozoan Fluorescent Protein Genes.
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ da
EMBL; AY679107; AAU04444.1; -; mRNA.
GO, GO:0006091; P:generation of precursor metabo
InterPro; IPR011584; GFP_related.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PFD01375; GFP; 1.
PFD00m; PP013756; Green fl_protein; 1.
PFD00m; PD013756; Green fl_protein; 1.
PFD00m; PD013756; Green fl_protein; 1.
               Wiedenmann Submitted (
                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
0range fluorescent protein FP586.
Discosoma sp. JW-2002.
Eukaryota, Metazoa; Cnidaria; Anthozoa; Zoan
Discosomatidae; Discosoma.
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25-OCT-2004 (TREMBLrel. 28, Last sequence up
25-OCT-2004 (TREMBLrel. 28, Last annotation
Enhanced red fluorescent protein R+.
Discosoma sp. RC-2004.
Eukaryota, Metazoa; Cnidaria; Anthozoa; Zoan
Discosomatidae; Discosoma.
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                                                                                                                     Discosomatidae; Di
NCBI_TaxID=208461;
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Q6KF85;
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               n J., Girod
(SEP-2002)
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Pred. No. 3.9e-95;
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Carter R.W., Gibbs P.D.L., Schmale M.C.;

"Cloning of Anthozoan Fluorescent Protein Genes.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databas

EMBL; AY679106; AAU04443.1; -; mRNA.

R GO; GO:0006091; P:generation of precursor metabolites

InterPro; IPR011584; GFP_related.

R InterPro; IPR010786; Green_fl_protein.

R Pfam; PF01353; GFP; 1.

R PFAM; PF01329; GFLUORESCENT.

R PFODOm; PD013756; Green fl_protein; 1.

SEQUENCE 236 AA; 27042 MW; BB38444BCD6834EF3 CRC64
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Best Local Similarity
Matches 221; Conserv
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Best Local :
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D8_9CNID
Q66ND8_9
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Discosoma sp. RC-2004.
Eukaryota; Metazoa; Cn
Discosomatidae; Discos
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25-OCT-2004 (TrEMBLrel.
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P42212; 1B9C.
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Last sequence update)
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Pred. No. 6.7e
1; Mismatches
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Pred. No. 1.1e-94;
2; Mismatches 3
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E151D0E497AA23FA CRC64;
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HSSP; Q9U6Y8; P:generation of precursor me!
GO; GO:0006091; P:generation of precursor me!
InterPro; IPR011584; GFP_related.
InterPro; IPR000786; Green_fl_protein.
PFGam; PF01353; GFP; 1.
R PRINTS; PR01259; GFLUORESCENT.
SEQUENCE 230 AA; 26370 MW; 5215B1B436D6'
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Best Local Similarity
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MEDLINE=20434599; PubMed=10981720; DOI=10.1016/S0014-5793(00)01895-0; Fradkov A.F., Chen Y., Ding L., Barsova E.V., Matz M.V., Lukyanov S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma sp. SSAL-2000.
Eukaryota, Metazoa, Cnidaria,
Discosomatidae, Discosoma.
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Q9GTJ7;
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PubMed=15556995; DOI=10.1073/pnas.0407752101; Wang L., Jackson W.C., Steinbach P.A., Tsien R.Y.; "Evolution of new nonantibody proteins via iterative somatic
                                                                     NUCLEOTIDE SEQUENCE
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88.1%; Pred. No. 1.3;
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Best Local S
Matches 185
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Best Local Similarity
Matches 181; Conserv
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Proc. Natl. Acad. Sci. U.S.A. 101:16745-16749 (2004).

EMBL; AY96536; AAV65486.1; -; mRNA.

GO; GO:0006091; P:generation of precursor metabolites
InterPro; IPR011584; GFP related.
InterPro; IPR011586; Green fl protein.

Pfam; PF01353; GFP; 1.
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01-FEB-2005 (TrEMBLrel. 29,
01-FEB-2005 (TrEMBLrel. 29,
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Eukaryota; Metazoa; Cnidaria;
Discosomatidae; Discosoma.
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PRODOm; PD013756; Green_fl_protein;
SEQUENCE 226 AA; 25513 MW; 159AV
                                                                                                                                                                                                                                                                                          InterPro; IPR011584; GFP related.

InterPro; IPR010786; Green_fl_protein.

Pfam; Pf01353; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

ProDom; PD013756; Green_fl_protein; 1.

SEQUENCE 226 AA; 25590 MW; 6DF38CAD2AB28BED CRC64;
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Q5S3G7;
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GO:0006091; P:generation of precursor
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IMYGSKAYVKHPADI PDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKV
                                         FQYGSKVYVKHPADIPDYKKLSFPBGFKWBRVMNFBDGGVVTVTQDSSLQDGCFIYKVKF 124
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Last annotation update)
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Pred. No. 6.3e-77;
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Pred. No. 8.4e-76;
8; Mismatches 28;
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		Search comple Job time : 74	Qy 125 Db 126 Qy 185 Db 186
		Search completed: January 11, 2006, 02:09:49 Job time : 74 secs	5 IGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAK 184

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; Sequence 12, Application US/09866538

; Patent NO. 6852849
; GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGET
APPLICANT: Campbell, Robert
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGEN1530-2
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 225
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No.
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; TYPE: PRT
; ORGANISM: Discosoma
US-09-866-538-12
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—Maximum Match 100%
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seq length: 2000000000
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Match Length DB
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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Copyright (c) 1993 - 2006 Compugen Ltd
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US-10-152-296-2
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Sequence 12, Appl
Sequence 2, Appli
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RESULT 3
US-10-152-296-2
; Sequence 2, Application US/10152296
; Patent No. 6723537
; Patent INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Peelle, Beau
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Directed Evolution of Protein in PTI.R REFERENCE: 021044-000110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOPTWARE: PATENTIN VERSION 3.0
SEQ ID NO 12
LENGTH: 225
TYPE: PRT.
ORGANISM: Discosoma sp.
US-09-865-291-12
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APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEM, ROGER
APPLICANT: TING, Alice
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS
FILE REFERENCE: REGEN1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1214; DB 2; Best Local Similarity 100.0%; Pred. No. 3e-132; Matches 225; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/152,296
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/291,871
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
FEATURE:
FEATURE:
Search completed: January 11, 2006, 02:10:50 Job time: 23 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:mammalian OTHER INFORMATION: codon-optimized variant (DsRED) of Discosoma sp. OTHER INFORMATION: "red" red fluorescent protein (RFP) US-10-152-296-2
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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1516.316 Million cell updates/sec
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-665-38-12
US-09-7494-308-12
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US-10-066-922-12
US-10-069-922-12
US-10-121-258-1
US-10-1315-920-2
US-10-315-920-2
US-10-313-640-13
US-10-313-640-13
US-10-845-948-13
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## ALIGNMENTS

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RESULT 1

US-09-999-745-67

(Sequence 67, Application US/09999745

; Sequence 67, Application US/09999745

; Patent No. US20020157120A1

; Patent No. US20020157120A1

; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL PERMOTER OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: The REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Baird, Geoffrey

TITLE OF INVENTION: CHRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS

PILE REFERENCE: REGEN1470-1

CURRENT APPLICATION NUMBER: US/09/999,745

CURRENT FILING DATE: 2001-10-23

PRIOR APPLICATION NUMBER: 09/316,920

PRIOR APPLICATION NUMBER: 09/316,920

PRIOR APPLICATION NUMBER: 09/316,920

PRIOR OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.0

SEQ ID NO 67

LENCTH: 225

TYPE: PRT

CRGANISM: Discosoma sp.
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RESULT 3
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APPLICANT: CENTEN, ROBET
APPLICANT: CENTENCE! ROBET
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGEN1530-2
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 12
LENGTH: 225
TYPE: DET
                                                                                                                                                         Sequence 12, Application US/09794308 Publication No. US20030170911A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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TSIEN, Roger
ZACHARIAS, David
BAIRD, Geoffrey
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                                                                                                                             REGENTS OF THE UNIVERSITY OF CALIFORNIA
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CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
SOPTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 225
TYPE: PRT
ORGANISM: Discosoma sp.
US-09-794-308-12
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09865291

Publication No. US20030186229A1

GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, Roger
APPLICANT: TING, Alice
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF
FILE REFERENCE: REGEN1550

CURRENT APPLICATION NUMBER: US/09/865,291

CURRENT FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 42

SOSTWARE: Patentin version 3.0

SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                          LENGTH: 225
TYPE: PRT
ORGANISM: Discosoma sp.
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APPLICANT: LIAVANOV, Sergey A
APPLICANT: LABAS, Yulii A.
APPLICANT: LABAS, Yulii A.
APPLICANT: LABAS, Yulii A.
APPLICANT: Terakikh, Alexey
APPLICANT: Terakikh, Alexey
TITLE OF INVENTION: No. US20020197676A1el Chromophores and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/444 118
Sequence 8, Application US/10081864

Publication No. US20030022287A1

GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushevich, Yuriy
APPLICANT: Yanushevich, Yuriy
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. US20030022287A1 Aggregating Flu
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067

CURRENT APPLICATION NUMBER: US/10/081,864

CURRENT FILING DATE: 2002-06-19
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PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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ORGANISM: Discosoma species
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; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma s
US-10-081-864-8
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, NAME/KEY: misc feature
; LOCATION: (1)...(225)
; OTHER INFORMATION: wild-type DsRed
US-10-121-258-1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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SEQ ID NO 1
SENGTH: 225
TYPE: PRT
ORGANISM: Discosoma sp.
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Best Local Similarity
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                                                                                                                                                    Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING:
FILE REFERENCE: UC083.1CF2CF1
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
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PRIOR FILING DATE: 2001-02-21
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                        61 LSPQFQYGSKYYVKHPADIPDYKKLSPPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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Conservative 0
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100.0%; Pred. No. 6.6e-114;
tive 0; Mismatches 0;
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Pred. No. 6.6e-114;
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; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-315-920-2
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Publication No. US20030203355A1
GENERAL INFORMATION:
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SEQ ID NO 4
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                                      APPLICANT: Bradbury, Andrew
APPLICANT: Zeytun, Ahmet
APPLICANT: Waldo, Geoffrey
APPLICANT: Waldo, Geoffrey
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fluorobodies: Binding Ligands With
TITLE OF INVENTION: Fluorescence
FILE APPLICATION NUMBER: US/10/132,067
CURRENT APPLICATION NUMBER: US/10/132,067
CURRENT FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 48
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APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS
TITLE OF INVENTION: FOR THEIR USE
FILB REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
NOTTABLE: FABUSEQ for Windows Version 4.0
                        SOFTWARE: PatentIn
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Pred. No. 6.6e-114;
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US-10-370-570-56
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CURRENT FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
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Best Local :
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Best Local Similarity 100.0%;
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TYPE: PRT
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YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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Pred. No. 6.6e-114;
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RESULT 11
US-10-406-618-32
Sequence 32, Application US/10406618
Sequence 32, Application US/20406618
; Publication No. US20030219814A1

GENERAL INFORMATION:

APPLICANT: Wan, APPLICANT: Ip, APPLICANT: The

David Chi-Cheong Denis Tsz-Ming Chinese University of Hong Kong

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LENGTH: 225
TYPE: PRT
RORANISM: Artificial Sequence
REATURE:
PERTURE:
OTHER INFORMATION: Description of Artificial Sequence: Spontaneously
OTHER INFORMATION: fluororescent protein DsRed.
US-10-406-618-32
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Publication No. US20040115792A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
YEAST STRAIN FOR TESTING THE GENOTOXICITY AND CYTOTOXICITY OF
TITLE OF INVENTION: COMPLEX ENVIRONMENTAL CONTAMINATIONS
FILE REFERENCE: 1487/3
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: DCT/EF01/14610
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: DE 10061872.3
PRIOR FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 225
TYPE: PRT
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Best Local
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CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: US 60/387,968
PRIOR FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/370,598
PRIOR PILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
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FILE REFERENCE: 016285-34-1
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Discosoma
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                                                                                                                                                           Similarity
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                                                                                                                                        100.0%; Score 1214; DB 4; ilarity 100.0%; Pred. No. 6.6e-114; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.6e-114;
tive 0; Mismatches 0;
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; LENGTH: 225
; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: synthetic construct
US-10-311-030-7
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
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Best Local Similarity 100.0%; P
Matches 225; Conservative 0;
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APPLICANT: Bulina, Maria
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APPLICANT: Telen, Roger
TITLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS
FILE REFERENCE: 15916-032US1
CURRENT APPLICATION NUMBER: US/10/311,030
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/US01/04625
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
APPLICANT: Chudakov, Dmitry
APPLICANT: Lukyanov, Konstantin
TITLE OF INVENTION: Mutant Chromaphores/Flourophores and
TITLE OF INVENTION: Methods for Making and Using the San
FILE REFERENCE: CLON 092
CURRENT APPLICATION NUMBER: US/10/845,484
CURRENT APPLICATION NUMBER: 004-05-12
PRIOR APPLICATION NUMBER: 60/343128
PRIOR FILING DATE: 2001-12-26
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Pred. No. 6.6e-114;
); Mismatches 0;
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; ORGANISM: Discosoma
US-10-885-988-12
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; ORGANISM: Discosoma sp
US-10-845-484-3
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PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOPTWARE: Patentin version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/10885988

Sequence 12, Application US/10885988

Publication No. US20040259165A1

GENERAL INFORMATION:

APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGEN1530-2

CURRENT APPLICATION NUMBER: US/10/885,988

CURRENT FILING DATE: 2004-07-06

CURRENT FILING DATE: 2004-07-06
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PRIOR FILING DATE: 2002-12-23
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 225
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Best Local Similarity
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APPLICANT: NEGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: SIEN, ROGER
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: Emission Ratiometric Indicators of
FILE REFERENCE: 39754-0891 CPC1CP2
CURRENT APPLICATION NUMBER: US/10/857,622
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: US 09/865,291
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR APPLICATION NUMBER: US 594,575
PRIOR APPLICATION NUMBER: US 594,575
PRIOR FILING DATE: 1996-01-31
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; ORGANISM: Discosoma
US-10-656-029-22
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                                                 SOFTWARE: FASTSEQ
SEQ ID NO 12
LENGTH: 225
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CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: 60/408,297
PRIOR FILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentin version 3.2
SEQ ID NO 22
LENGTH: 225
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publication No. US20050003367A1
GENERAL INFORMATION:
APPLICANT: VERTEX PHARMACEUTICALS INC.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RAPID DEVELOPMENT
TITLE OF INVENTION: SCREENING ASSAYS
FILE REFERENCE: VPI/02-143WO2
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                                                                                                            NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
ORGANISM: Discosoma
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PRIOR APPLICATION NUMBER: UP 2002-45728
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: UP 2002-213949
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: UP 2002-298237
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 233
SEQ ID NO 26
FENORED 2002-10-11
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US-10-505-486-26
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; Sequence 2, Application US/10844064A
; Publication No. US20050149994A1
; GENERAL INFORMATION:
; APPLICANT: Bevis, Brooke
; APPLICANT: Glick, Benjamin
; TITLE OF INVENTION: RAPIDLY MATURING FLUORESCENT PROTEINS AND METHODS FOR USING THE
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TYPE: PRT

ORGANISM: Discosoma sp.
US-10-505-486-26
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US-10-844-064A-2
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Publication No. US20050118539A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries,
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Best Local Similarity
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TITLE OF INVENTION: WONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/21,258
PRIOR PILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/21,258
PRIOR PILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 225
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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
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Best Local (
Query Match 100.0%; Score 1214; DB 5; Length 225; Best Local Similarity 100.0%; Pred. No. 6.6e-114; Matches 225; Conservative 0; Mismatches 0; Indels 0
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CURRENT APPLICATION NUMBER: US/10/844,064A
CURRENT FILING DATE: 2004-05-11
PRIOR APPLICATION NUMBER: PCT/US02/40539
PRIOR FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US 60/341,723
PRIOR FILING DATE: 2001-12-19
                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(225)
OTHER INFORMATION: wild-type DsRed
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Discosoma
                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                       ENGTH: 225
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Sequence 1, Application US/10343977

Publication No. US20050112682A9

GENERAL INFORMATION:
APPLICANT: Kuhlemann, Rene
APPLICANT: Kottermann, Andre
APPLICANT: Kettling, Ulrich
APPLICANT: Schwille, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Autofluorescent fusion protein derived from GFP; OTHER INFORMATION: e.g. Aequorea victoria and/or Discoma sp. US-10-343-977-1
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APPLICANT: Koltermann, Andre
APPLICANT: Koltermann, Andre
APPLICANT: Koltermann, Andre
APPLICANT: Schwille, Petra
TITLE OF INVENTION: Dual coloured fluorimetric pro
FILE REFERENCE: 023425us/JH/ml
CURRENT APPLICATION UNMBER: US/10/343,977
CURRENT APPLICATION NUMBER: DO3-02-06
PRIOR APPLICATION NUMBER: PCT/EP01/09112
PRIOR TILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 12
SOTTWARE: Patentin Ver. 2.1
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US-10-343-977-1
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US-10-343-977-1
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Best Local
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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CURRENT APPLICATION NUMBER: US/10/343,977
CURRENT FILING DATE: 2003-02-06
FRIOR APPLICATION NUMBER: PCT/EP01/09112
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 12
SOPTWARE: PAtentin Ver. 2.1
SEQ ID NO 2
LENGTH: 506
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US-10-343-977-2
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APPLICANT: Kuhlemann, Rene
APPLICANT: Koltermann, Andre
APPLICANT: Kettling, Ulrich
APPLICANT: Schwille, Petra
TITLE OF INVENTION: Dual coloured fluorimetric
FILE REFERENCE: 02342518/JH/ml
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FILE REFERENCE: 023425us/JH/ml
CURRENT APPLICATION NUMBER: US/10/343,977
CURRENT FILING DATE: 2003-02-06
PRIOR APPLICATION NUMBER: PCT/EP01/09112
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
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Best Local :
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Best Local :
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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                                                                                                                              100.0%; Score 1214; DB 4; ilarity 100.0%; Pred. No. 2e-113; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1214; DB 5; ilarity 100.0%; Pred. No. 1.9e-113; Conservative 0; Mismatches 0;
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APPLICANT: Koltermann, Andre
APPLICANT: Kettling, Ulrich
APPLICANT: Kettling, Ulrich
APPLICANT: Kettling, Ulrich
APPLICANT: Schwille, Petra
TITLE OF INVENTION: Dual coloured fluorimetric pro
FILE REFERENCE: 023425ug/JH/ml
CURRENT APPLICATION NUMBER: US/10/343,977
CURRENT FILING DATE: 2003-02-06
PRIOR APPLICATION NUMBER: PCT/EP01/09112
PRIOR APPLICATION NUMBER: PCT/EP01/09112
PRIOR APPLICATION NUMBER: PCT/EP01/09112
SOPTWARE: PATENTING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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                                                                                                                                                                                                Sequence 3, Application US/10343977 Publication No. US20040014134A1 GENERAL INFORMATION:
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Best Local (
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            APPLICANT: Kuhlemann, Rene
APPLICANT: Kuhlemann, Andre
APPLICANT: Koltermann, Andre
APPLICANT: Koltermann, Andre
APPLICANT: Koltermann, Andre
APPLICANT: Koltermann, Andre
APPLICANT: Schwille, Petra
TITLE OF INVENTION: Dual coloured fluorimetric
FILE REFERENCE: 023425u8/JH/ml
CURRENT APPLICATION NUMBER: US/10/343,977
CURRENT FILING DATE: 2003-02-06
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TYPE: PRT
ORGANISM: Artificial sequence
PEATURE:
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APPLICATION NUMBER: PCT/EP01/09112
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APPLICANT: Koltermann, Andre
APPLICANT: Kettling, Ulrich
APPLICANT: Schwille, Petra
TITLE OF INVENTION: Dual coloured fluorimetric protease assay
FILE REFERENCE: 023425us/JH/ml
CURRENT APPLICATION NUMBER: US/10/343,977
CURRENT FILING DATE: 2003-02-06
PRIOR APPLICATION NUMBER: PCT/EP01/09112
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 12
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 547
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US-10-343-977-3
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Best Local S
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kuhlemann, Rene
APPLICANT: Koltermann, And
APPLICANT: Kettling, Ulri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-08-07 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Autofluorescent fusion protein derived from OTHER INFORMATION: e.g. Aequorea victoria and/or Discoma sp.
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 547
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                                                                                                                                                                                                          / Match 100.0%; Score 1214; DB 5; Local Similarity 100.0%; Pred. No. 2.2e-113; les 225; Conservative 0; Mismatches 0;
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                                                                                                                                                                  1 MRSSKUVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
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                                                                                   LSPQFQYGSKVYVKHPADIPDYKKLSFPBGFKWBRVMNFEDGGVVTVTQDSSLQDGCFIY 120
KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI
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Pred. No. 2.2e-113;
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GENERAL INFORMATION:

APPLICANT: Nelson, David

APPLICANT: Zamiars, Elize

APPLICANT: Tsien, Roger

TITLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS

FILE REFERENCE: 15916-032US1

CURRENT APPLICATION NUMBER: US/10/311,030

CURRENT FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: PCT/US01/04625

PRIOR PILING DATE: 2001-02-13

PRIOR APPLICATION NUMBER: US 60/184,732

PRIOR APPLICATION NUMBER: US 50/184,732

PRIOR FILING DATE: 2000-02-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 226
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US-10-152-296-2
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US-10-311-030-9
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                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10152296
Publication No. US20030077730A1
GENERAL INFORMATION:
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                                                           SEQ ID NO 2
                                                               APPLICANT: Pedile; Beau
APPLICANT: Pedile; Beau
APPLICANT: Rigel pharmaceuticals, Incorporated
TITLE OF INVENTION: Directed Evolution of Protein in Mammalian
FILE REFERENCE: 021044-000110US
CURRENT APPLICATION NUMBER: US/10/152,296
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/291,871
PRIOR FILLING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
ORGANISM: Artificial Sequence
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                                    ENGTH:
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Pred. No. 1.7e-113;
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APPLICANT: Peelle, Beau
APPLICANT: Rigel Pharmaceuticals, Incorporated
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITIE OF INVENTION: Directed Evolution of Protein
FILE REFERENCE: 021044-000110US
CURRENT APPLICATION NUMBER: US/10/739,656
CURRENT FILING DATE: 2003-12-17
PRIOR APPLICATION NUMBER: US/10/152,296
PRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/291,871
PRIOR TILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 2
SOUTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10739656 Publication No. US20040126850A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Matches 224;
                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:mammalian OTHER INFORMATION: codon-optimized variant (DsRED) of Discosoma OTHER INFORMATION: "red" red fluorescent protein (RFP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                        LSPQFQYGSKVYVKHPADI PDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFI Y
YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
                                                     KVKF1GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE1HKALKLKDGGHYLVEFKS1
                                                                                                                                LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 121
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99.6%;
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99.6%;
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Pred. No. 1.8e-113;
1; Mismatches 0;
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Pred. No. 1.8e-113;
1; Mismatches 0;
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YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL

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APPLICANT: HWANG, Inhwan
APPLICANT: KIM, Dae Heon
APPLICANT: KEB, Yong Jik
ITILE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APB02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 52
LENGTH: 545
TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                        APPLICANT: HWANG, Inhwan
APPLICANT: KIM, Dae Heen
APPLICANT: LEE, Yong Jik
TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APB02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: Patentin version 3.1
SEQ ID NO 76
LENGTH: 548
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US-10-214-932-76
; Sequence 76, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION:
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US-10-214-932-52
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                                                                                                                                 ; OTHER INFORMATION: Synthetic Sequence US-10-214-932-76
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                                                          Matches
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Best Local Similarity
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                                                                                                                                                                                                              TYPE: PRT
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Local Similarity 99.6%;
hee 224; Conservative
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                                                            Conservative
                                                                            99.7%;
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                                                          Score 1210; DB 4;
Pred. No. 5.7e-113;
1; Mismatches 0;
                                                                                                Length 548;
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Sequence 4, Application US/10315920
Publication No. US20030175809A1
GENERAL INFORMATION:
APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Terskikh, Alexey
ITITLE OF INVENTION: FLUORESCENT TIMER PR
TITLE OF INVENTION: FOR THEIR USE
FILE REFERENCE: CLON-077CIP
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US-10-315-920-4
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US-10-121-258-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.4%;
Best Local Similarity 99.6%;
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APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR
FILE REFERENCE: UCO83.1CP2CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
CURRENT APPLICATION NUMBER: US/10/315,920
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pred. No. 3.3e-113;
0; Mismatches 1;
                                                        PROTEINS
                                                          AND
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APPLICANT: Telen, Roger
APPLICANT: Baird, Geoffrey
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAK
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/874,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-05-24
PRIOR PILING DATE: 2001-05-26
NUMBER: 09 SEQ ID NOS: 110
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PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 225
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US-10-931-304-20
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                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 225
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Publication No. US20050196768A1
                                                                   Matches
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                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                          FEATURE: OTHER INFORMATION: Dered with I125R
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ORGANISM: Artificial
FEATURE:
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Local Similarity 99.1%;
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                                                                                         Similarity
MRSSKOVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDI
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                                                                   Conservative
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                                                                                     99.4%;
                                                              Score 1207; DB 5;
Pred. No. 3.3e-113;
0; Mismatches 1;
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Pred. No. 3.3e-113;
1; Mismatches 1;
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                                                                                                         Length 225;
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                                                                   Indels
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Sequence 2, Application US/10314936

| Publication No. US20040110225A1
| GENERAL INFORMATION:
| APPLICANT: Gibbs, Patrick D.L.
| APPLICANT: Carter, Robert W.
| ITTLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
| FILE REFERENCE: 638.004
| CURRENT APPLICATION NUMBER: US/10/314,936
| CURRENT APPLICATION NUMBER: US/10/314,936
| CURRENT FILING DATE: 2002-12-09
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 2
| LENGTH: 236
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US-10-314-936-4
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APPLICANT: Gibbs, Patrick D.L.
APPLICANT: Carter, Robert W.
APPLICANT: Schmale, Michael C.
TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
FILE REFERENCE: 638.004
CURRENT APPLICANTION NUMBER: US/10/314,936
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                             Sequence 4, Application US/10314936
Publication No. US20040110225A1
GENERAL INFORMATION:
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ORGANISM: Artificial
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Sequence 2. Application US/11021014

Publication No. US20050100954A1

(PENERAL INFORMATION:
APPLICANT: Glabbe, Patrick D.L.
APPLICANT: Carter, Robert W.
APPLICANT: Schmale, Michael C.
ITITE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
FILE REFERENCE: 638.004

CURRENT APPLICATION NUMBER: US/11/021,014

CURRENT FILING DATE: 2004-12-23

PRIOR APPLICATION NUMBER: US/10/314,936

PRIOR APPLICATION NUMBER: US/10/314,936

PRIOR APPLICATION NUMBER: US/10/314,936

PRIOR APPLICATION NUMBER: US/10/314,936

PRIOR FILING DATE: 2002-12-09

NUMBER OF SEQ ID NOS: 15

SOPTWARE: Patentin version 3.1

SEQ ID NO 2
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Best Local Similarity
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TYPE: PRT
ORGANISM: Artificial
FEATURE:
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TYPE: PRT
ORGANISM: Artificial
FEATURE:
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Local Similarity 98.2%;
nes 221; Conservative :
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                                                                                                    KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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                    YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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Pred. No. 4.6e-112;
2; Mismatches 2;
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Pred. No. 4.6e-112;
2; Mismatches 2;
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APPLICANT: Carter, Robert W.
APPLICANT: Schmale, Michael C.
TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQU
FILE REFERENCE: 638.004
CURRENT APPLICATION NUMBER: US/11/021,014
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: US/10/314,936
PRIOR PILLING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3:1
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APPLICANT: MacDonald, Marnie
APPLICANT: MacDonald, Marnie
APPLICANT: Lamerdin, Jane
TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PR
TITLE OF INVENTION: COMPLEMENTATION ASSAYS
FILE REFERENCE: ODDY007
CURRENT APPLICATION NUMBER: US/10/724,178
CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: US 60/461,133
PRIOR FILING DATE: 2003-04-09
NUMBER OF SEQ. ID NOS: 1067
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LENGTH: 236
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Publication No. US20050100954A1
                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/10724178 Publication No. US20040137528A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Odyssey Thera, Inc. APPLICANT: Michnick, Stephen
                NAME/KEY: misc feature
OTHER INFORMATION: Discosoma red
PUBLICATION INFORMATION:
AUTHORS: Matz, M.V. et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: mutant red fluorescent protein
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                                                                                                                                      ORGANISM: Anthozoa discosoma;
                                                                                                                                                         LENGTH: 226
TYPE: PRT
TITLE: Fluorescent proteins from nonbioluminescent Anthozoa species
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98.2%;
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Pred. No. 4.6e-112;
2; Mismatches 2;
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FULL REFERENCES: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
FRIOR PPLICATION NUMBER: 607/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-315-920-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PAGES: 969-73; DATE: 1999-
; RELEVANT RESTOUES: (1)..(226)
US-10-724-178-12
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Best Local Similarity 99.1
Marches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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                        181
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                                                                                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVATVTQDSSLQDGCFIY
                                                                                                                                                                             LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                              KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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99.1%;
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Pred. No. 4.9e-112;
0; Mismatches 1;
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                                                                                                                                                               NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 239
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
Query Match
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APPLICANT: HIROTA, KIYONORI
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND
TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME
FILE REFERENCE: 04583.0103-0000
CURRENT APPLICATION NUMBER: US/10/442,148A
CURRENT FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: JP 2002-148950
PRIOR FILING DATE: 2002-05-23
                                                                                                                                                                                                                                                         APPLICANT: IWAKURA, MASAHIRO
APPLICANT: HIROTA, KIYONORI
TITLE OP INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND
TITLE OP INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAM
FILE REFERENCE: 04583.0103-00000
CURRENT APPLICATION NUMBER: US/10/442,148A
CURRENT FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: JP 2002-148950
PRIOR FILING DATE: 2002-05-23
                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein sequence
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Local Similarity 97.3%;
nes 219; Conservative
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  Score 1186;
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Pred. No. 4.4e-111;
2; Mismatches 4; Indels
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Length 239;
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APPLICANT: Tesien, Roger

APPLICANT: Campbell, Robert

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

FILE REFERENCE: UC083.1CP2CP1

CURRENT APPLICATION NUMBER: US/10/121,258

CURRENT FILING DATE: 2002-04-10

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 225
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                                                                         RESULT 44
US-10-931-304-4
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Publication No. US20030059835A1
GENERAL INFORMATION:
Sequence 4, Application US/10931304
Publication No. US20050196768A1
GENERAL INFORMATION:
APPLICANT: Teien, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.6%; Score 1160; I
Best Local Similarity 96.0%; Pred. No. 1.8e
Matches 216; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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2; Mismatches 4;
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       Query Match
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RESULT 45

US-10-121-258-24

(Sequence 24, Application US/10121258)

Publication No. US20030059835A1

Publication No. US20030059835A1

GENERAL INFORMATION:
APPLICANT: Tsien, Roger

ITILE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

FILE REFERENCE: UC083.1CP2CP1

CURRENT APPLICATION NUMBER: US/10/121,258

CURRENT FILING DATE: 2002-04-10

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-931-304-4
; OTHER INFORMATION: DsRed polypeptide variant US-10-121-258-24
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PRIOR FILLING DATE: 2002-07-29
PRIOR PELICATION NUMBER: 10/121,258
PRIOR FILLING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILLING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILLING DATE: 2001-02-26
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                                                                                                                                     SEQ ID NO 24
LENGTH: 225
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APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: WONDERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: WONDERIC AND METHODS FOR MAKING SAME
FILE REFERENCE: 39754-0831CP2CP3
CURRENT PEPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
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ORGANISM: Artificial Sequence
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                                                       ORGANISM: Artificial Sequence FEATURE:
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96.0%; Pred. No. 1.8e-108;
tive 3; Mismatches 6;
                                  "T1" with I125R mutation
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Score 1153;

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APPLICANT: TSIEN, ROGER
APPLICANT: Campbell, Robert
APPLICANT: BAITG, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND METHODS FOR MAK.
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: U9/10/931,304
CURRENT APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-05-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 225
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Publication No. US20050196768A1
                                                                                                                                                                                                                                                                                                                                                                      Matches
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181
                                                                                                                     121 KVKPIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDCGHYLVEFKSI 180
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                            YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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YMAKKPVOLPGYYYVDSKLDITSHNEDYTIVEQYERAEGRHHLFL 225
                                                                                      KVKFRGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                             MASSEDVIKEPMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 1153; DB 5; Length 225; 95.6%; Pred. No. 9.4e-108; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 9.4e-108; 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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CURRENT APPLICATION UNMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 226
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US-10-121-258-6
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                                                                                            ; OTHER INFORMATION: DsRed polypeptide variant "dimer2" US-10-121-258-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-423-688A-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10121258 Publication No. US20030059835A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/423,688A
CURRENT FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: 10/132,067
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2
SEQ ID NO 41
SEQ ID NO 41
Query Match
Best Local Similarity
Matches 207; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Los Alamos National Laboratory
APPLICANT: Waldo, Geoffrey S.
TITLE OF INVENTION: Directed Evolution Methods for Improving Polypeptide Folding and
TITLE OF INVENTION: Solubility and Superfolder Fluorescent Proteins Generated Thereby
FILE REFERENCE: S-100,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING
FILE REFERENCE: UC083.1CP2CP1
                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Discosoma
                                                                                                                                                                                       TYPE: PRT
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                        92.3%;
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                        Score 1121; DB 4; Length 226; Pred. No. 1.6e-104;
       Indels
    <u>,</u>
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    Gaps
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RESULT 47

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APPLICANT: TSIEN, ROGET
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAK
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 226
TYPE: PRT
ORGANISM: Artificial Sequence
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// FEATURE:

// OTHER INFORMATION: DeRed polypeptide variant "dimer2"

US-10-931-304-6

                                                       US-11-052-001-6
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Publication No. US20050196768A1
GENERAL INFORMATION:
Sequence 6, Application US/11052001 Publication No. US20050233356A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                             PQFQYGSKVYVKHPADIFDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKV 122
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                                                                                                                                                                                                                                                                                                                             SSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILS
                                                                                                                         AKKPVQLPGYYYVDTKLDITSHNEDYTIVEQYERSEGRHHLFL 226
                                                                                                                                              AKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                         92.3%;
                                                                                                                                                                                                                                                                                                                                                                                             Score 1121; DB 5;
Pred. No. 1.6e-104
7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                          LENGTH: 225
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APPLICANT: Lukyanov, Sergey A
APPLICANT: Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Terskikh, Alexey
ITITE OF INVENTION: No. US20020197676A1el Chromophores and
ITITE OF INVENTION: Wethods for Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JONES, JOSHUA T.
APPLICANT: HAHN, ANGELA TERESA
APPLICANT: MEYER, TOBIAS
TITLE OF INVENTION: LIVE-CELL BIOSENSOR POLYPEPTIDES AND
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
TILE REFERENCE: STAN-385
CURRENT TILING DATE: 2005-02-03
CURRENT TILING DATE: 2005-02-03
PRIOR APPLICATION NUMBER: 60/541,297
PRIOR FILLING DATE: 2004-02-03
NUMBER OF SEG ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: fluorescent fusion protein US-11-052-001-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44, Application US/10006922 Publication No. US20020197676A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 602
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 92.3%;
Local Similarity 92.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1121; DB 6;
Pred. No. 6.1e-104;
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APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushevich, Yuriy
APPLICANT: Yanushevich, Yuriy
APPLICANT: Savistky, Alexandr
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT APPLICATION NUMBER: 10/06,922
PRIOR APPLICATION NUMBER: 10/06,922
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-081-864-12
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; OTHER INFORMATION: hybrid construct
US-10-006-922-44
                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: hybrid protein US-10-081-864-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/10081864 Publication No. US20030022287A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 225
TYPE: PRT
                                                                                                                                                                                                                                                                                          y Match 92.2%; Score 1119; DB 4;
Local Similarity 91.6%; Pred. No. 2.5e-104;
hes 206; Conservative 12; Mismatches 7;
                       181
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                                                                                                                                       13
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                                                                                                                                                                                                                                        MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRSSKNVIKEFMRPKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
                                                                                 KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                                                     LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSCSKNVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVIKGGPLPFAFDI
YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                           MSCSKNVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY
                                                                                                                                       LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY
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Pred. No. 2.5e-104;
12: Mismatches 7;
                                                                                                                                                                                                                                                                                                                              Length 225;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tsien, Roger

APPLICANT: Tsien, Roger

APPLICANT: Gampbell, Robert

APPLICANT: Balid, Geoffrey

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: MONOMERIC VARIANTS AND METHODS FOR MAI

FILE REFERENCE: 39754-0831CP2C93

CURRENT APPLICATION NUMBER: US/10/931,304

CURRENT FILING DATE: 2004-08-30

PRIOR APPLICATION NUMBER: 10/209,208

PRIOR APPLICATION NUMBER: 10/209,208

PRIOR PILING DATE: 2002-07-29

PRIOR PILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: 10/121,258

PRIOR APPLICATION NUMBER: 09/866,538
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APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FL
TITLE OF INVENTION: PROTEIN VARIANTS AND ME
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/894,308
PRIOR APPLICATION NUMBER: 09/894,308
PRIOR FILING DATE: 2011-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2011-02-26
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Best Local S
Matches 201
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SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                           Sequence 106, Application US/10931304
Publication No. US20050196768A1
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Publication No.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: DsRed polypeptide variant "dimer2.2MMM (dimer3) (dtomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 91.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 FMYGSKAYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGLVTVTQDSSLQDGTLIYKVKM 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPVQLPGYYYVDTKLDITSHNEDYTIVEQYERSEGRHHLFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQYGSKYYYKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEVIKEFMRFKVRMEGSMNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10931304
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Pred. No. 7e-102;
8; Mismatches 12;
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METHODS FOR MAKING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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Sequence 18, Application US/10006922

| Publication No. US20020197676A1
| GENERAL INFORMATION:
| APPLICANT: Likyanov, Sergey A
| APPLICANT: Fradkov, Arcady F.
| APPLICANT: Fradkov, Arcady F.
| APPLICANT: Habs, Yulii A.
| APPLICANT: Matz, Mikhail V.
| APPLICANT: Terekikh, Alexey
| TITLE OF INVENTION: No. US20020197676A1el Chromophores and
| TITLE OF INVENTION: Methods for Using the Same
| FILE REFERENCE: CLON-035CIP
| CURRENT APPLICATION NUMBER: US/10/006,922
| CURRENT FILING DATE: 2001-12-04
| PRIOR APPLICATION NUMBER: 09/120,330
| PRIOR APPLICATION NUMBER: 09/457,898
| PRIOR APPLICATION NUMBER: 09/457,898
| PRIOR APPLICATION NUMBER: 09/458,144
| PRIOR APPLICATION NUMBER: 09/458,144
| PRIOR APPLICATION NUMBER: 09/458,477
| PRIOR APPLICATION NUMBER: 
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PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 106
LENGTH: 476
TYPE: PRI
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US-10-931-304-106
                                                                                                                                       US-10-006-922-18
                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 18
LENGTH: 230
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Best Local Similarity
Query Match
Best Local Similarity
Matches 199, Conserv
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                                                                                                                                                                      TYPE: PRT
ORGANISM: Discosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVIKEFMR FKVRMEGSMNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGFLFFAMDILSPQ
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      Conservative
                                                                                                                                                                  species
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91.0%; Pred. No. 1.9e-101;
tive 8; Mismatches 12;
   89.4%; Score 1085.5; DB 4; Length 230;
88.1%; Pred. No. 6.2e-101;
Live 17; Mismatches 9; Indels 1;
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APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/10161403 Publication No. US20030119104A1
                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Discosoma species
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
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                                                                                                                                                        61 LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSPOPQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY 120
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                                                                                    KVKFIGVNFPSDGPVMQKKTMGWBASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                                                                                                                    LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIY
                                                                                                                                                                                                           MSCSKNVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI
YMVKKPSVQLPGYYYVDSKLDMTSHNEDYTVVEQYEKTQGRHHPFI
                  YMAKKP-VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
                                                                  EVKFIGVNFPSDGÞVMQRRTRGWEASSERLYPRDGVLKGDIHMALRLEGGGHYLVEFKSI
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                                                                                                                                                                                                                                                                                 89.4%; Score 1085.5; DB 4
88.1%; Pred. No. 6.2e-101;
tive 17; Mismatches 9;
                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                       230;
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RESULT 57 US-11-006-076-40

Sequence 40, Application US/11006076
Publication No. US20050181506A1
GENERAL INFORMATION:
APPLICANT: Perkins, Edward

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APPLICANT: Eleming, Elema
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION. CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 17084-022002/420B
CURRENT APPLICATION NUMBER: US/11/006,076
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 40
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US-10-006-922-46
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; TYPE: PAT
; ORGANISM: Discosoma species
US-11-006-076-40
                                                                                       CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR PRILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR PRILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR PRILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-035CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lukyanov, Sergey A
APPLICANT: Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
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APPLICANT:
APPLICANT:
                     PRIOR APPLICATION NUMBER: 09/444,338 PRIOR FILING DATE: 1999-11-19 NUMBER OF SEQ ID NOS: 46
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FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YMAKKP-VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225
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Leung, Josephine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.4%; Score 1085.5; DB 6
88.1%; Pred. No. 6.2e-101;
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APPLICANT: Tsien, Reger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAI
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
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US-10-121-258-8
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 192
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Publication No. US20030059835A1
GENERAL INFORMATION:
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Best Local Similarity 87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 205
TYPE: PRT
ORGANISM: Discosoma species
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                  181 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
181
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                                                                                                                                                                                                                               1 MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                          KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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                                                                                                                                                   LSPOTOYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTODSSLQDGEFIY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL
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                                                                        KVKLRGTNFPSDGPVMQKKTMGWEASTERMYPEDGALKGEIKMRLKLKDGGHYDAEVKTT
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Pred. No. 5.1e-97;
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APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
ITILE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
ITILE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAR
FILE REFERENCE: 39754-0831CP2C93
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/794,308
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publication No. US20040137528A1
GENERAL INFORMATION:
APPLICANT: Odyssey Thera, Inc.
APPLICANT: Michaick, Stephen
APPLICANT: MacDonald, Marnie
APPLICANT: Lamezdin, Jane
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US-10-724-178-16
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FILE REFERENCE: ODDYOO7

CURRENT APPLICATION NUMBER: US/10/724,178

CURRENT FILING DATE: 2003-12-01

PRIOR APPLICATION NUMBER: US 60/461,133

PRIOR FILING DATE: 2003-04-09

NUMBER OF SEQ ID NOS: 1067

SOFTWARE: Patentin version 3.0

SEQ ID NO 16

LENGTH: 225

TYPE: PRT

ORGANISM: Artificial

FEATURE:

FEATURE: PRT

ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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Publication No. US20050196768A1
NUMBER OF SEQ ID NOS: 110
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 225
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86.9%; Pred. No. 1.9e-94;
vative 5; Mismatches 24; Indels
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DSRED polypeptide variant "mGrapel"
US-10-931-304-108
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PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 108
LENGTH: 225
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Best Local Similarity 86.9%;
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PRIOR FILING DATE: 2002-07-29
PRIOR PELICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
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ORGANISM: Artificial Sequence
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Local Similarity 86.4%;
nes 191; Conservative 6
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                                                                        LSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGBFIY
                                                                                                                                                       MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDI
                          KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
  KVKLRGTNFPSDGPVMQKKTMGWEASSERLYPEDGALKGEIKMRLKLKDGGHYDAEAKTT 180
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                                                                                                                                                                                                                              Score 1014; DB 5; Length 225; Pred. No. 9.8e-94; 6; Mismatches 24; Indels
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US-10-931-304-79
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US-10-931-304-104
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US-10-931-304-79
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLITILE OF INVENTION: PROTEIN VARIANTS AND METERIC REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
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                                                                                                                                                                                                                                Sequence 104, Application US/10931304 Publication No. US20050196768A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 225
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Publication No. US20050196768A1
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PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
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TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
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APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
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ORGANISM: Artificial Sequence
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86.0%;
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Pred. No. 1.6e-93;
                                                                                              FLUORESCENT
METHODS FOR
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RESULT 65
US-10-931-304-100
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                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 100 LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 100, A. Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                         Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR
FILE REFERENCE: 39754-0831CP2CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                            OTHER INFORMATION: Daked polypeptide variant "mTangerine'
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nes 188; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LSPQFMWGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIY 120
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1 MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFÄWDI 60
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o. US20050196768A1
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85.1%;
                                         6
                                                            Score 1002;
Pred. No. 1.6
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Pred. No. 5e-93;
8; Mismatches 25;
                                           Mismatches
                                         ; DB 5;
1.6e-92;
nes 26;
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                                                                               Length 225;
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MAKING SAME

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APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
ITILE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
ITILE OF INVENTION: MONOMERIC AND METHODS FOR MAK.
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-26
INUMBER OF SEQ ID NOS: 110
SOCTWARE: PRESENCE FRANCE: PRESENCE TYPE: PRI
TY
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US-10-931-304-85
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US-10-931-304-89
, Sequence 89, Application US/10931304
; Publication No. US20050196768A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: DeRed polypeptide variant "OrS4-9"
US-10-931-304-85
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Best Local Similarity
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                                                                                                                                                                                                                                                                       VOLPGYYYVDSKLDITSHNBDYTIVEQYBRTBGRH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIXKVKLRG
                                                                                                                                                                                                                TNPPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKMRLKLKDGGHYDAEVKTTYKAKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.9%; Score 994; DB 5; Length 236; 86.5%; Pred. No. 1.1e-91;
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PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 89

LENGTH: 236

TYPE: PRT
ORGANUS: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dered polypeptide variant "mFRFP (F2Q6) (mGrape2)"

US-10-931-304-89
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APPLICANT: Campbell, Robert

APPLICANT: Campbell, Robert

APPLICANT: Campbell, Robert

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

FILE REFERENCE: 39754-083102CP3

FURRENT APPLICATION NUMBER: US/10/931,304

CURRENT FILING DATE: 2004-08-30

PRIOR APPLICATION NUMBER: 10/209,208

PRIOR FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: 10/21,258

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR APPLICATION NUMBER: 09/866,538
                                                                                                                                                       APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAI
FILE REFERENCE: 39754-0831C92C93
FILE REFERENCE: 39754-0831C92C93
FILE REFERENCE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 2001-05-26
PRIOR PILING DATE: 2001-05-26
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US-10-931-304-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                      SOFTWARE: FASTSEQ
SEQ ID NO 102
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 TNFPSDGPVMQKKTMGWEASSERLYPEDGALKGEVKMRLKLKDGGHYDAEVKTTYMAKKP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 VNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKÞ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102, Application US/10931304 ton No. US20050196768A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VIKBEMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDILSPQFQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGSKAYVKHPPDIPDYMKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLHG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQLPGAYKLDYKLDITSHNEDYTIVEQYERAEGRH 226
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                                                                                                          for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 992; DB 5; L
Pred. No. 1.7e-91;
6; Mismatches 24;
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US-10-931-304-83
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US-10-931-304-83
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CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR PILLING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILLING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILLING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILLING DATE: 2001-02-26
PRIOR FILLING DATE: 201-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 83
LENGTH: 236
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                  Query Match
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Best Local Similarity 86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR FILE REFERENCE: 39754-0831CP2CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
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                                                           127 VNFPSDGPVMOKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKP 186
                                                                                                       72
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                                                                                                                                                                                                                                                                          184;
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                                                                                                                                                                                                                                7 VIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQ 66
                                                                                                                               YGSKVYVXHPADIPDYKXLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIG
                                                                                                                                                                                      IIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKMRLKLKDGGHYTSEVKTTYKAKKP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGSKAYVKHPADIPDYFKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRG
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                   TNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKP
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                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                            81.4%;
85.6%;
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Pred. No. 3.5e-91;
5; Mismatches 25;
                                                                                                                                                                                                                                                                        Score 988; DB 5;
Pred. No. 4.4e-91;
6; Mismatches 25
                                                                                                                                                                                                                                                                                                                  DB 5; Length 236
                                                                                                                                                                                                                                                                          25; Indels
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Sequence 94, Application US/10931304
Publication No. US20050196768A1
GENERAL INFORMATION:
APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
ITITLE OF INVENTION: MONOWERIC AND DIMERIC FLUORESCENT
ITITLE OF INVENTION: MONOWERIC AND DIMERIC FLUORESCENT
ITITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAP
ILLE REFERENCE: 39754-0831CF2CB3
CURRENT APPLICATION UNMBER: US/10/931,304
CURRENT APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
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US-10-931-304-92
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 92
LENGTH: 236
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PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
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APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
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CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/794,308 PRIOR FILING DATE: 2001-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: DsRed polypeptide variant "mRFP2 (mCherry)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
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No. US20050196768A1
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Pred. No. 5.6e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLUORESCENT
METHODS FOR
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APPLICANT: Token, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
ITILE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
ITILE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-02-26
NUMBER OF EGO ID NOS: 110
SOFTWARE: FASTSEQ for Windows Version 4.0
SECTION: DOT
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PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR PILING DATE: 2001-05-24
PRIOR PILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR PRIOR OF SEQ ID NOS: 110
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
LENCTH: 235
LENCTH: 235
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                                                                   ; FEATURE:
; OTHER INFORMATION: DSRED polypeptide variant "mROFP (A2/6-6)"
US-10-931-304-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-931-304-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 96, Applica publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 184; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: 62
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence PEATURE:
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                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 VNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKF 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQLPGAYIVGIKLDITSHNEDYTIVEQYERAEGRH 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10931304
No. US20050196768A1
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  Score 973; DB 5; Length 236; Pred. No. 1.4e-89;
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APPLICANT: BAIR, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLI
TITLE OF INVENTION: MONOMERIC SAND ME;
FILE REFERENCE: 39754-0831C92C93
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-26
PRIOR FILING DATE: 2001-02-26
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US-10-931-304-98
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 98
LENGTH: 236
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Publication No. US20050196768A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.1%;
Best Local Similarity 84.7%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 IIKEFMRFKVRMEGSVNGHEFEIEGEGEGERPYEGTQTAKLKVTKGGPLPFAWDILTFNFT 71
                                                                                                                                                                                                                                                                                                                    72 YGSKAYVKHPADIPDYLKLSFPEGFKWERVWNFEDGGVVTVTQDSSLQDGEFIYKVKLRG
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                                         VQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
                                                                                                                                                                                                           VNFPSDGFVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKF 186
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                                                                                                                                                              TNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKMRLKLKDGGHYDAEVKTTYKAKKP
                                                                                                                                                                                                                                                                                                                                                                     YGSXVYVKHPADIPDYKKISPPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIG 126
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VQLPGAYIVGIKLDITSHNEDYTIVELYERAEGRH
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Pred. No. 1.4e-89;
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METHODS FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 236
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RESULT 74 US-10-931-304-87

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Sequence 1041, Application US/10724178

Publication No. US20040137528A1

GENERAL INFORMATION:
APPLICANT: Odyssey Thera, Inc.
APPLICANT: MacDonald, Marnie
APPLICANT: MacDonald, Marnie
APPLICANT: MacDonald, Marnie
TITLE OF INVENTION: COMPLEMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
TITLE OF INVENTION: COMPLEMENTATION ASSAYS
FILE REFERENCE: ODDY007
CURRENT APPLICATION NUMBER: US/10/724,178
CURRENT APPLICATION NUMBER: US/0/461,133
PRIOR APPLICATION NUMBER: US 60/461,133
PRIOR APPLICATION SERIES OF SEG ID NOS: 1067
SOFTWARE: Patentin version 3.0

SEG ID NO 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/931,304
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR PRILING DATE: 2002-07-29
PRIOR PRILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR PRILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR PILING DATE: 2001-05-24
PRIOR PRILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 87
LENGTH: 236
TYPE: PRT
ORGANISM: Artificial Sequence
PRATIDE:
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US-10-724-178-1041
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; OTHER INFORMATION: DeRed polypeptide variant "Y1.3 (mYOFP 1.3)(mBanana)"
US-10-931-304-87
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Publication No. US20050196768A1

GENERAL INFORMATION:

APPLICANT: Taien, Roger

APPLICANT: Campbell, Robert

APPLICANT: Baird, Geoffrey

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

FILE REFERENCE: 39754-0831CP2CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.1%;
Best Local Similarity 83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 180; Conservative
TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                             ENGTH: 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGDLPFAWDILSPQFQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKMRLKLKDGGHYSAETKTTYKAKKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 960; DB 5; Length 236
Pred. No. 2.9e-88;
5; Mismatches 30; Indels
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Search completed: January 11, 2006, 02:12:06 Job time : 64 Becs
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Best Local (
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                                                                                                                                122
                                                                                                                                                   123 KFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYM 182
                                                                 182
                                                                                               183 AK 184
                                                                                                                                                                                                   62
                                                                                                                                                                                                                   63 PQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKV 122
                                                                                                                                                                                                                                                                                        3 SSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILS
                                                                                                                                                                                                                                                                   2 SSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILS
                                                                 AK 183
                                                                                                                                 KLRGTNFPSDGPVMQKKTMGWEASTERMYPEDGALKGEIKMRLKLKDGGHYDAEVKTTYM 181
                                                                                                                                                                                                   PQFQYGSKAYVKHPADIPDYLKLSFPEGFKWBRVMNFEDGGVVTVTQDSSLQDGEFIYKV 121
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                                                                                                                                                                                                                                                                                                                                              69.9%;
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Pred. No. 4.1e-77;
5; Mismatches 18
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Sequence 1, Application US/10209208
Publication No. US20050244921A1
GENERAL INFORMATION:
APPLICANT: Tsien, Reger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                  RESULT 1
US-10-209-208-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/USOS_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USOS_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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length: 2000000000
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99.4
95.6
95.0
92.3
83.4
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Match
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Gapop 10.0 , Gapext 0.5
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(without alignments)
212.341 Million cell updates/sec
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1214
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-209-208-20

US-10-209-208-24

US-10-209-208-6

US-10-209-208-6

US-10-209-208-7
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                                                                                    AND METHODS
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Sequence 20, Appl
Sequence 4, Appli
Sequence 24, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 79, Appl
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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.LCP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
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PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
                                                                           OTHER INFORMATION: DsRed with I125R US-10-209-208-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Publication No. US20050244921A1
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Best Local 9
Query Match
Best Local Similarity
Matches 224; Conserv
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TYPE: PRT
ORGANISM: Discosoma sp
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NAME/KEY: misc_feature
LOCATION: (1)...(225)
OTHER INFORMATION: wild-type DsRed
                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                 FEATURE:
                                                                                                                                                                        LENGTH: 225
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  Conservative
                  99.4%;
  0;
  Score 1207; DB 6;
Pred. No. 1.1e-109;
0; Mismatches 1;
                                      Length 225;
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MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60

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APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
ITILE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UCO83.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-26
NUMBER OF SEQ ID NOS: 80
SECTIMARE: FastSEQ for Windows Version 4.0
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Sequence 24, Application US/10209208
Publication No. US20050244921A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
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Best Local Similarity
Matches 216; Conserv
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Publication No. US20050244921A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1160; DB 6;
Pred. No. 3.7e-105;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 225;
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CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 226
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TITLE OF INVENTION: FLUCRESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
FRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/964,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 2001-05-26
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
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US-10-209-208-6
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 24
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10209208
Publication No. US20050244921A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.0%;
Best Local Similarity 95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FULDRESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tsien, Roger
                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DsRed polypeptide variant "dimer2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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 Mismatches

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Pred. No. 1.8e-104;
  Score 1121;
  BB
  6;
Length 226;
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APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC003.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR PILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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RESULT 7
US-10-209-208-79
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORCANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DBRed polypeptide variant "mRFP1"
10-209-208-8
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nes 207; Conservative
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nee 192; Conserv
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                                                                                                                                YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
                                                                                                                                                                                                           KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
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                                                                                                    YMAKKPVQLPGAYKTDIKLDITSHNEDYTIVEQYERAEGRH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                  84.1%; Score 1021; DB 6; Length 225; ilarity 86.9%; Pred. No. 1e-91; Conservative 5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.2e-101; 7; Mismatches 9;
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APPLICANT: TSIEN, ROGER
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FUORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 190; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
181
                                            181
                                                                                         121
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                                                                                                                                                                           61 LSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIY
                                                                                                                                                                                                          61 LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY 120
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                                                                                                                                                                                                                                                                                              1 MRSSKNVIKEFMRFKVRMEGTVNGHEFBIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI 60
                                                                                                                              KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI 180
                                     YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRH 221
                                                                                      KVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKMRLKLKDGGHYDAEVKTT 180
                                                                                                                                                                                                                                                                                                                                                         83.4%;
ilarity 86.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                           Score 1012; DB 6;
Pred. No. 7.4e-91;
6; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 225;
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Search completed: January 11, 2006, 02:12:24 Job time : 10 secs

Application US/10209208

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Result
No.
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-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q-/Ggn2 1/USPTO_Spool_p/US1006592/runat_10012006_162504_19114/app_query.fasta_1.391
-Q-/Ggn2 1/USPTO_Spool_p/US10065922/runat_10012006_162504_19114/app_query.fasta_1.391
-DB=GenEmb1 -QFMT=fastap -SUFFIX=p2nminscr.rge -MINMATCH=\overline{0.7} 1. -LOOPCL=0
-DB=GenEmb1 -QFMT=fastap -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=blts -START=1 -RND=-1 -MATRIX=blooum62 -ALIGN=500
-LIST=500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-69 -ALIGN=500
-MODE=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=\overline{0.7} -MAXLEN=200000000
-MODE=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=\overline{0.7} -MAXLEN=2000000000
-MODE=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -THRELOOF -LOOGLOG
-MODE=LOCAL -QUTFMT=0 - NORM=ext -HEAPSIZE=500 -TOOGLOG
-USER-US10006922 @CGN 1 17415 @runat 10012006 162504 19114 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPELOCK=100 -LOOGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEVEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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Tsien, R. Y. and Gonzalez, J.E. III.
Detection of transmembrane potentials
Patent: US 6342379-A 6 29-JAN-2002;
Location/Qualifiers
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Patent: WO 0142211-A 6 14-JUN-2001;
The Regents of the University of California
Location/Qualifiers
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                                    GACTATAAAAAGCTGTCATTTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACTTTGAA
                                              AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                               TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA
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/mol_type="unassigned DNA"
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Corallimorpharia; Discosomatidae; Discosoma.
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Sequence 13 from Patent
AX207715
AX207715.1 GI:15422399
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LeuSerProGlnPheGlnTyrGlySerLy8ValTyrValLy8HisProAlaAspIlePro
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                                   CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGACCTTTGCCATTTGCTTGGGATATT
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/mol_type="unassigned DNA"
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Corallimorpharia; Discosomatidae; Discosoma
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    ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                      MetArgSerSerLy8AgnValIleLy8GluPheMetArgPheLy8ValArgMetGluGly
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678 225 0

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Sequence 1 from Patent W00196373.
AX370404 GI:18857490
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                                                                                                                                                                                                                                       sequences; artificial sequences.
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/noTe="variant of sequence from
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoar
Corallimorpharia; Discosomatidae; Discosoma
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Discosoma sp.

Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;

Corallimorpharia; Discosomatidae; Discosoma.

1 (bases 1 to 859)

Matz,M.V., Fradkov, A.F., Labas, Y.A., Savitsky, A.P., Z

Markelov, M.L. and Lukyanov, S.A.

Fluorescent proteins from nonbioluminescent Anthozoa
                                                                                                      AF168419
Discosoma sp. fluorescent
AF168419
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                                                                                 Discosoma sp.
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Matz,M.V., Fradkov,A.F., Labas,Y.A., Savitsky,A.P.,
Markelov,M.L. and Lukyanov,S.A.
Direct Submission
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Matz,M.V., Fradkov,A.F., Labas,Y.A., Savitsky,A.P.,
Markelov,M.L. and Lukyanov,S.A.
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1 (bases 1 to 859)
1 sien,R.Y., Ting,A.Y. and Zhang,J.
Emission ratiometric indicators of phosphorylation Patent: US 6900304-A 11 31-MAY-2005;
The Regents of the University of California; Oakla Location/Qualifiers
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AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
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Corallimorpharia, Discosomatidae, Discosoma.
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US-10-006-922A-12 (1-225) x AX463698 (1-859)
                                                                                                      Nelson,D., Zamanra,...

Modified fluorescent proteins
Patent: WO 0162919-A 8 30-AUG-2001;
Aurora Biosciences Corporation (US)
Location/Qualifiers
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                                                TyrMetAlaLysLysProValGlnLeuProGl
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Unlien,E., Mauchamp,B., Nony,P., Prudhomme,J.C. and Royer,C.
Nucleic acid controlling the expression of a useful polypeptide in
the posterior silk glands of a lepidoptera and application thereof
Patent: WO 2004083445-A 1 30-SEP-2004;
Centre National De La Recherche
CLAUDE BERNARD - LYON 1 (FR); Institut National de la Recherche
Agronomique (INRA) (FR)
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GACGGCGGCGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
            AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
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Centre National De La Recherche Scientifique-CNRS (FR); UNIVERSITE CLAUDE BERNARD LYON 1 (FR); Institut National de la Recherche
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence
AX463702
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Lichtenberg-Frat, Hella (DE)
Location/Qualifiers
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Yeast strain for testing
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/noCe="Vektor pDsRed1-N1"
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                                                                                                                                                                                                         synthetic construct
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                                                                                                                                                                                                          sequences; artificial sequences.
/note="MPSV 5'-LTR 997. .1014
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                                                1. .435
                                                                                                                      Location/Qualifiers
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                             | IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
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                                                                                                                                                                             MetGlyTrpGluAla8erThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
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                                                                                                                                                               /note="eGFP(tag)-Gen a
3164. 4019
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4081. 4641
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1015. 1560
1561. 1599
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1600. 2289
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complement (707. .1387)

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GREFALROPAGNCVHFVAEEQD"
complement(2860. 2992)
/note="SV40 polyA"
complement(3066. 4097)
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VKLKVTKGGLIPBAMDILSPOROKSIXVVKHENDIDDGVLKSSPERT
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   complement (5151.
                                    complement (4745. .4762)
                                                  /note="internal ribosome entry sequence
encephalomyocarditis virus"
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US-10-006-922A-12 (1-225) x AY569779 (1-8811)
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161 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
                                                                                                                          MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
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                                                                                                                                                                                                          AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACC
                                                                                                                                                                                                                                              LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                                                                                                                                                                                                                                      GACGGCGGCGTGACCGTGACCCAAGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC 1025
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     AY569780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crerceccaerrecaeraceecrecaaeereracereaaecaececeeceaeareece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                                                                                                                                                                                                                               MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                                            ATCACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGC
                                                                                                                                                                   IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                                                                                                                                                                                                     IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGGCGGCGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                        CACCACCTGTTCCTG
                                                                                                       HisHisLeuPheLeu 225
                                                                                                                                                                                                               TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC
                                                                                                                                                                                                                                         TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
                                                                                                                                                                                                                                                                                  ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
                                                                                                                                                                                                                                                                                                                                                         ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="EGFP-EJ, abgeleitet von EGFP (Clontech, Palo Alto, CA, USA)" 5527. 9320 /note="Retroviraler Vektor p5NM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MVRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDILSPQPFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTEBLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERT
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Matches:
Conservative:
Mismatches:
Indels:
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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-MAR-2004) Fish Genetics, Inc
Chinese Academy of Science, 7# South Road
Hubei 430072, People's Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning vector pTCCR-Auto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning vector pTCCR-Auto, complete sequence. AY569780
AY569780.1 GI:45861238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 12404)
Wu,G., Wang,Y. and Zhu,Z.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other sequences; artificial sequences; vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SV40 polyA"
complement(707. .1387)
/codon_start=1
/transT_----
                                                                                                                                                                                                                                                                                                                                                                                    /translation="MANLLTVHQNLPALPVDATSDEVRKNLMDMFRDRQAFSEHTWKM
LLSVCRSWAAWCKLNNRKWFPASPEDVRDYLLYLQARGLAVKTIQQHLGQLNMLHRRS
GLPRESDSNAVSLVWRRIFKKENVDAGERAKÇALAFERTPDQVRSLMESBDRCQDIRD
LAPLGIAYNTLLRIAEIARIRVKDISRTDGGRMLIHIGRTKTLVSTAGVEKALSLGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1447. .2036)
/note="CMV promoter"
complement (2387. .2761)
                                                                                                                                                                               /note="T7 promoter"
complement(4837. .4967)
                                                                                                                                                                                                                                                 encephalomyocarditis virus"
                                                                                                                                                                                                                                                                         complement(4109. .4683)
/note="internal ribosome entry sequence from
                                                                                                                                                                                                                                                                                                                        MVRLLEDGD"
                                                                                                                                                                                                                                                                                                                                         KLVERWI SVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTRALEGI FEATHRLI YGAK
DDSGQRYLAWSGHSARVGAARDMARAGVSI PEIMQAGGWTNVNI VMNYI RNLDSETGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3066. .4097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (2860. .2990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVTLFISAVQDQVVPDNTLAMVMVRGLDELYAEWSEVVSTNFRDASGPAMTEIGEQPW
GREFALRDPAGNCVHFVAEBQD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mvrssknvikefmrfkvrmegtvnghefeiegeggegrpyeghnt
vklkvtkggplpfamdilspqfqygskvyvkhpadipdykklsppegfkmervmnfed
ggvvtvtqdsslqdgcfiykvkfigvnfpsdgpvmqkktmgmeasterlyprdgvlkg
                  /product="T7 RNA polymerase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="zeocin"
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/bb_xref="GI:45861240"
/translation="MAKLTSAVPVLTARDVAGAVEFWTDRLGFSRDFVEDDFAGVVRD
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/mol_type="other DNA"
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                                                                                                                                                          note="T7 terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAS78502.1"
/db_xref="GI:45861241"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="T7 terminator"
translation="MNTINIAKNDFSDIBLAAIPFNTLADHYGERLAREQLALEHESY
                                                                                                               codon start=1
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                                                                                                                                                                                                                            lement (4745. .4762)
                                                                                                                                  ement (5009. .7660)
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US-10-006-922A-12 (1-225) x AY569780 (1-12404)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                          1324 ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCCGAGGGCCGCCCTACGAGGGC 1265
                                                                                                                                                                                                             1384 GTGCGCTCCTACCAAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
41 HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60
                                                                                                                            21 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                                                                                                                                                                                  1 MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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FIGKBGYYMLKIHGANGAGUDKVPFPERIKFIEDHIHMIMACAKS PLENTWMARQDSP
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HEKYGIESFALHDSFGTIPADAANLFKSVKRTETMVDTYESCDVLADFYDQFADQLHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mkpvtlydvabyagvsyqtvsrvvnqashvsaktrekveaamae
Lnyipnrvaqqlagkqslligvatsslalhapsqi'vaaiksplolgasvvvsavers
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Edsscyippsttikqdfrilgqtsvdrllqlsqqqavkgnqllpvslvkrkttlapnt
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/note="internal ribosome entry sequence
encephalomyocarditis virus"
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FQFLQEIKPEAVAITIKTLACLTSADMISYVASAIGRAIEDEARFGRIRDLEAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="Amp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
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/db_xref="GI:45861243"
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Matches:
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MctArgSerSerLy8AsnValIleLy8GluPheMetArgPheLy8ValArgMetGluGly
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/db_xref="taxon:32630"
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Odenthal, Margarete (DE)
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         Odenthal, M. and Jung, D. Gene expression, genome alteration and myofibroblast-like Patent: WO 0204509-A 22 17-JAN-2002; Odenthal, Margarete (DE)
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Discosoma sp. RC-2004
Discosoma sp. RC-2004
Eukaryota, Metazoa; Cnidaria; Anthozoa; Zoantharia;
Corallimorpharia; Discosomatidae; Discosoma.
1 (bases 1 to 711)
Carter, R.W., Gibbs, P.D.L. and Schmale, M.C.
Cloning of Anthozoan Pluorescent Protein Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-JUL-2004) MBF, CBWY, Miami, FL 33129, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter, R.W., Gibbs, P.D.L. and Schmale, M. Direct Submission
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                              MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                         LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
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Discosoma sp. JW-2002
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Corallimorpharia; Discosomatidae; Discosoma.
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                                           ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                   ATGAGTTGTTCCAAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGTATGGAAGGA
 HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                               (bases 1 to 678)
                                                                                                                                                                                                                                                                                                       /product="orange fluorescent protein PP586"
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/tanslation="MSCSKNVIKEFWRFKVRMEGTVNGHEFBIEGEGEGRPYGGHNTV
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GVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGD
IHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTE
                                                                                                                                                                                                                                                                                                                                                                                                                       fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Discosoma sp.
/mol_type="mRNA"
/db_xref="taxon:208461"
/note="isolated from spe
                                                                                                                                                                                                                                                                                            GRHHLFL"
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                                                                                                                                                                                                                                                                                                          synthetic construct
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                                                                                                                                                                       organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"
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                                                                                                                                                              note="variant
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                                                                                                                                                aggregating fluorescent proteins ent: WO 02068459-A 14 06-SEP-2002;
                                                                                                                                                                                              sequences; artificial
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/mol type="unassigned DNA"
/db xref="taxon:32630"
/noTe="non-aggregating mutant"
                                                                                                                                   Location/Qualifiers
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Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoanthe Corallimorpharia; Discosomatidae; Discosoma.
1 (bases 1 to 921)
Carter, R.W., Gibbs, P.D.L. and Schmale, M.C.
Cloning of Anthozoan Fluorescent Protein Genes
2 (bases 1 to 921)
Carter, R.W., Gibbs, P.D.L.
Direct Submission
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TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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IHKALKLKDGGHYLVEFKTIYMAKKPVQLPGYYYVDSKLDITSHNKDYTIVEQYERTE
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other sequences; artificial sequences
                                                               Ly8ValLy8PheIleGlyValAsnPheProSerAspGlyProValMetGlnLy8Ly8Thr
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AX666133
AX666133.1 GI:29290961
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Anticancer, Inc. (US)
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  LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
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/mol_type="unassigned DN
/db_xref="taxon:32644"
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AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                  GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                       AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                              CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
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DB:
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Pred. No.:
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       ThrvalAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
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                                                              CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGCCCCCTGCCCTTCGCCTGGGACATC
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Cloning vector pSAT6-DsRed2-C1,
AY818375
AY818375.1 GI:56553574
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                                                                                                                                                                                                                                        Tzfira,T., Lacroix,B. and Citovsky,V.
Direct Submission
Submitted (05-NOV-2004) Department of Biochemistry
Biology, State University of New York Stony Brook,
Stony Brook, NY 11794, USA
Location/Qualifiers
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Cloning vector pSAT6-DsRed2-C1
Other sequences; artificial sec
1 (bases 1 to 4546)
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                                          HisHisLeuPheLeu 225
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DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDMMEADKVAGPL
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complement(3486. .4346)
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Best Local Similarity:
Query Match:
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                                                                   US-10-006-922A-12 (1-225) x DQ005468 (1-4555)
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Direct Submission
Submitted (12-APR-2005) Department of
Biology, State University of New York
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Chung, S.-M., Vyas, S. and Tzfira, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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A versatile vector system for multiple gene expression in plants
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Cloning vector pSAT6A-DsRed2-N1
                                                                                                                                                                                                                                                      /translation="MSIQHERVALIPFFAAFCLPVFAHPETIVKVKDAEDQLGARVGY IELDLASGKILESFREEERFPMMSTFKVLLCGAVLSRIDAGGEQLGRRIHYSQNDLVE YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLITTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALFAGWFIADKSGAGERGSRGIIAALGFDGKPSRIVVIYTTGSQATMDERNRQIA EIGASLIKHW"
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1321.
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441. .762
                                                                                                                                                                                                                                                                                                                                                                                                               /note="CaMV 35S terminator"
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GVATVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE
THKALKLKDGGHYLVEFKSIYMAKKFVQLPGYYYVDAKLDITSHNEDYTIVEQYERTE
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1380. .2057
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768. .1089
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                                                                                                                                                                                                                                                                                                                                                               protein_id="AAY25373.1"
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                                                                                                                                                                                                                                                                                                                                   AY818373 4570 bp
Cloning vector pSAT6-DgRed2-N1,
AY818373
AY818373.1 GI:56553569
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Cloning vector pSAT6-DsRed2-N1
other sequences; artificial sequences; vectors.
                                                          Submitted (05-NOV-2004) Department of Biology, State University of New York Stony Brook, NY 11794, USA Location/Qualifiers
                                                                                                                    Tzfira, T., Lacroix, B. and Citovsky, V. Direct Submission
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/organism="Cloning vector
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/note="CaMV 35S terminator"
complement(3510. .4370)
/note="amp resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="massenvitefmrfkvrmegtvnghefbiegegggrpyeghntvkkkvrkggplpfamdilspqpqygskvyvkhpadipdykklsppegfkwervmnfedggvatvtqdsslqdgcfiykvkfigvnfpsdgfvmqkktmgweasterlyprdgvlkgg
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/note="CaMV 35S promoter"
768. .1090
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IELDLNSGKLILSERRPEBERPFMMSTFKVLLGAVLGAVLGARIPLAMMGDHVTRL
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLLDWMEADKVAGPL
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/note="5' UTR
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/db_xref="GI:56553571"
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/note="multiple
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Michel, U., Malik, I., Ebert, S., Bahr, M. and Kugler, S.
Long-term in vivo and in vitro AAV-2-mediated RNA interference
rat retinal ganglion cells and cultured primary neurons
Biochem. Biophys. Res. Commun. 326 (2), 307-312 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 siRNA vector pSUPER-hSyn-DsRed2N1-CytB-AS
siRNA vector pSUPER-hSyn-DsRed2N1-CytB-AS
other sequences; artificial sequences; vec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-MAY-2004) Neurology, Un:
Waldweg 33, Goettingen 37073, Germany
Location/Qualifiers
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Michel, U. and Kuegler, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="siRNA vector
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/db_xref="taxon:297630"
135.441
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                                                                                                    /tranelation="MASSENVITEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTV
KLKVTKGGFLPFAWDILSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDG
GVATVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKIMGWEASTERLYPRDGVLKGE
                                                                                                                                                                                                                                                                                                         complement (739. .899)
/notee "SV40-pA; SV40 polyadenylation sequence"
complement (899. .1039)
/notee "SV40 chimeric intron derived from pCI-NI
complement (1045. .1722)
                                                  complement (1741. .1759)
                                                                                      THKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDAKLDITSHNEDYTIVEQYERTE
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                                                                                                                                                    /transI_table=11
/product="DsRed2"
/protein_id="AAV73958.1"
/db_xref="GI:56119186"
                                                                                                                                                                                                                                                                                           /gene="DsRed2"
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                                                                                                                                                            LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
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   ACCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
                         IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                         MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
                                                                                                                                        GACGGCGGCGTGGCCACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
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2240. 2455

/note="disabled human H1 RNA

2456. 2587

/note="Cytb-AS; partial human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="beta-lactamase"
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/protein id="AAV73959.1"
/db xref="g1:56119187"
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LRSALPAGMFTADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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/codon_start=1
/transl_table=11
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Michel, U., Malik, I., Ebert, S., Bahr, M. and Kugler, S.
Long-term in vivo and in vitro AAV-2-mediated RNA interference rat retinal ganglion cells and cultured primary neurons
Blochem, Biophys. Res. Commun. 326 (2), 307-312 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIRNA Vector pSUPER-CMV-DBRedZN1-CytB-AS, complete sequence. AY640625
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Michel, U. and Kuegler, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DeRed2"
/codon_start=1
/transI_table=1
                                                                                                                                            complement (1741. .1760)
/note="MCS'; multiple cloning site"
complement (1771. .2293)
/note="MCMV promoter; mcmv promoter (-491
2294. .2309
                                                                                                                                                                                                                                                                                                                                    /protein_id="AAV73952.1"
/db_xref="G1:56119177"
/db_xref="G1:56119177"
/tranelation="MASSENVITEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTV
/tranelation="MASSENVITEFMRFKVRWEGTVNGHEFEIEGEGEGRPYEGHNTV
KLKVTKGGFLFPAWDILSPQFOYGSKVYVKHPADIEDYKKLSFPEGFKWERVMFEDG
KLKVTKGGFLFPAWDILSPQFOYGKVKFIGVNFPSDGPVNQKKTMGWEASTERLYPRDGVLKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (739. .899)
/note="SV40-pA; SV40 polyadenylation sequence"
complement (899. 1039)
/note="SV40 chimeric intron derived from pCI-NI
complement (1045. .1722)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="siRNA vector pSUPER-CMV-DsRed2N1-CytB-AS"
/mol_type="other DNA"
/db xref="taxon:297627"
1357..441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="derived from Clontech's complement(1045. .1722)
             /note="disabled human H1 RNA promoter"
2533. .2664
/note="Cytb-AS; partial human cytochro
                                                                                                                                                                                                                                                                                                              THKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDAKLDITSHNEDYTIVEQYERTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="DsRed2"
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                                                                                                                        note="MCS'; multiple cloning site"
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                                                                                                                                                                                                        IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                                                                                                                                                                                                                                                                   MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                                                                                                                                                                                     AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTGATGCAGAAGAAGAACC
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IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg 220
                                                                                  TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp 200
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YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDMMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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3103. .3770
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/protein_id="AAV73953.1"
/db_xref="GI:56119178"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
Query Match:
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AJ851284.1 GI:55724874
DB Red fluorescent protein
CLoning vector pRU1104
CLoning vector pRU1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-OCT-2004) Poole P.S., School of AMS, University Reading, Whiteknights, Reading, RG6 6AJ, UNITED KINGDOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poole, P.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karunakaran, R. and Poole, P.S.
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LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                               HisasnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                                                                                                                                                               ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
                                                                                                                           ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                                                                                                                   MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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KLKVTKGGFLPFAMDILSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDG
GVATVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGE
                                                                                                                                                                                                                                                                                                                                                                                                      THKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDAKLDITSHNEDYTIVEQYERTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transT_table=11
/product="Ds Red fluorescent protein
/protein_id="CAH64889.1"
/db_xref="GI:55724875"
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db_xref="taxon:299179"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning vector pSRalphaneoR Cloning vector pSRalphaneoR other sequences; artificial 1 (bases 1 to 6423)
                                                                                                                                                                                                                                                                                Submitted (01-MAY-2004) INRS-Institut
Boulevard des Prairies, Laval, Quebec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY613997 6423
Cloning vector pSRalphaneoR,
AY613997
AY613997.1 GI:48995616
                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 6423)
Allard, V., de Leseleuc, L. and Denis, F.
                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                        A family of mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HisHisLeuPheLeu
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/codon_start=1
/transT_table=11
/product="red fluorescent p
/protein_id="AAT46428.1"
/db_xref="GI:48995617"
                                                                                                                                                                                             /organism="Cloning vector
/mol_type="other DNA"
/db_xref="taxon:279783"
100. .686
                                                                                                                                     1431. .2108
                                                                                                                                                                                                                                                                     Location/Qualifiers
    translation="MASSENVITEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTV/
                                                                                                        431. .2108
                                                                                                                    gene="dsRED2"
                                                                                                                                                   note="ECMV internal"
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f mammalian expression vecto
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H7V 1B7, Canada
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                                                      AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
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/codon_start=1
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/protein_id="AAT48429 l"
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/the protein_id="Reported in the protein id="Reported in the protein in the prote
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THKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDAKLDITSHNEDYTIVEQYERTE
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/product="ampicillin resistance protein"
/protein id="AA748430.1"
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/translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARIHYSQNDLVE
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TELDLNSGKTLESFRPESERFPMMSTFKVLLCGAVLSRVDAGGGDLIDMWEADKVAGFL
LRWALIPAGMFTADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
LRWALIPAGMFTADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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/note="SRalpha"
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SiRNA vector pAAV9(5)-hSyn-DsRed2N1-EGFP-siRNA, complete sequence.
AY640634
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-JUN-2004) Neurology, Waldweg 33, Goettingen 37073, Germa Location/Qualifiers
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Michel, U., Malik, I. and Kuegler, S.
Direct Submission
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1 (bases 1 to 6990)
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             /db_xref="GI:56119204"
/translation="massenvitefmrfkvrmegtvnghefbiegegegrpyeghntv/translation="massenvitefmrfkvrmegtvnghefbiegegegrpyeghntvkxvxxkggplpfamdilspqpqygskvyvkhpadipdykklspegegkmervmnfeddgvatvtqdsslqdgcfiykvkfigvnfpsdgvmqkktmgmbasterlyprdgvlkgb
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/mol type="other DNA"
/db xref="taxon:297636"
/complement(38. .193)
                                                                                                                                                                              /gene="DsRed2"
/note="derived from Clontech's pDsRed2-N1"
complement(348. .1025)
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complement(198. .341)
THKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDAKLDITSHNEDYTIVEQYERTE
                                                                                                                         /gene="DsRed2"
/codon_start=1
/transl_table=11
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/protein_id="AAV73970.1"
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cultured primary neurons
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                                                                                                                                                                                                                                                                21
                                                    AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                    AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                                                     LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                                                       HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                                                                                                                                                                                                                                                        ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
                                                                                                                                                                                                                                                                                         ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
                                                                                                                                                                                                                                                                                                      MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
                                                                                     GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                       CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
                                                                                                                                                                                       CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCCTTCGCCTGGGACATC
                                                                                                                                                                                                                                                                                                                                        (1-225) x AY640634 (1-6990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY IBLDLASGKILESFREEER PMSIFKYLLCGAVLSTRLDAGGEDGRRIHYSQNDLVE YSPVTEKHLFOGMTVBELCSAAITMSDNTAAILLTTIGEDFRELTAFLHMGDHVTEL DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDMMEADKVAGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="partial sequence
9(5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="HSYN-promoter; human synapsin 1 gene promoter (-422 to +53)" 1543. .1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6848. .6988
/note="left ITR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIGASLIKHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Amp"
5167. .6027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="siEGFP; 64 bp siRNA sequence" complement(1827. .4090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MCS; multiple cloning complement (1062. .1531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1044. .1062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="beta-lactamase"
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/note="ampicillin resistance"
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AY640633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Michel, U., Malik, I., Ebert, S., Bahr, M. and Kugler, S. tong-ferm in vivo and in vitro ALV-2-mediated RNA interference rat retinal ganglion cells and cultured primary neurons Biochem. Biophys. Res. Commun. 326 (2), 307-312 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            siRNA vector pAAV9(5)-hSyn-DsRed2N1-CytB-AS-ohneNot siRNA vector pAAV9(5)-hSyn-DsRed2N1-CytB-AS-ohneNot other sequences; artificial sequences; vectors.

1 (bases 1 to 7058)
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SiRNA vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACGTGGACGCCAAGCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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/db_xref="G1:56119202"
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/translation="MASSENVITEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTV
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complement(38. .193)
/note="SV40-pA', SV40 polyadenylation sequence"
complement(198. .341)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="siRNA vector
pAAV9(5)-hSyn-DsRed2N1-CytB-AS-ohneNot"
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complement (1187. .1205)
                            GRHHLFL"
                                                                                                                                                                                                                                                                                                                                                             complement (491 .1168)
                                                                                                                                                                                                                                                                                                                                                                                          complement (491. .1168)
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1. .141
                                                                                                                                                                                                                                                                                                            /note="derived from Clontech's
                                                                                                                                                                                                                                                                                                                                      /gene="DsRed2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="left ITR"
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                                                                                                                                                                                                                 CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                    ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
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                                                                                                                                                      GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
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complement(1205. .1674)
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/gene="Amp"
/note="ampicillin resistance"
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/note="Cytb-AS; partial human cytochrome B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="HSYN-promoter; human synapsin 1 gene promoter (-422
to +53)"
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/rpt_family="inverted"
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RESULT 41
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Michel, U., Malik, I. and Kuegler, S.
Direct Submission
Submitted (01-JUN-2004) Neurology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michel, U., Malik, I., Ebert, S., Bahr, M. and Kugler, S. Long-term in vivo and in vitro AAV-2-mediated RNA interference rat retinal ganglion cells and cultured primary neurons Biochem. Biophys. Res. Commun. 326 (2), 307-312 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY640630 7147 bp DNA circular SYN 01-JUL-2005 SiRNA vector pAAV9(5)-CMV-DBRedZN1-CYtB-AS-ohneNot, complete
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siRNA vector pAAV9(5)-CMV-DsRed2N1-CytB-AS-ohneNot
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (181. .338)
/note="SV40-pA'; SV40 polyac
complement (341. .481)
/note="SV40 chimeric intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="siRNA vector
pAAV9(5)-CMV-DsRed2N1-CytB-AS-ohneNot"
/mol_type="other DNA"
                                                                                                                                                   /traibiation="massenvitepmrfkvmmegtvngheffiegegegrpyeghntvkuktyrgeghippm".ktkvtkgeghypkymyktymghastbaltpegegegrpyeghntvkuktyrgeghippmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoyktgaphpmidispopoy
                         /note="MCS'; multiple cloning site"
complement(1217. .1739)
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/gene="DsRed2"
                                                                                            complement (1187.
                                                                                                                                                                                                                                                                      /product="DsRed2"
/protein_id="AAV73963.1"
/db_xref="GI:56119193"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="DsRed2"
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Best Local Similarity:
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                                          MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
                                                                                            LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                                                                                                                                                                                                                              HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60
IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                                                                                                              AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
                                                                                                                                                                                    GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                                                                                                                       CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
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                                                                                                                                 GACGGCGGCGTGGCCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
                                                                                                                                                                                                  AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                                                                                                                                                                                         CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCTGCCCTTCGCCTGGGACATC
                                                                                                                                                                                                                                                                                                                                                                                               ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
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/rpt_family="inverted"
5467. .6327
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/product "beta-lactamase"
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/db.xref="Qil:56119192"
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TELDLNSGKILESFRPEERFPMNSTFKVLLCGAVLSRLDAGDEGGRRLHYSQNDLVE
YSPVTEKHLTOGMTVRELCGAAITMSONTAANLLLTTIGGELTAFLHMWGDHVTRL
DRWEPELNEAIPNDERDTTMFVAMATTLRKLLTGELTTLASRQQLIDMMEADKVAGPL
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/note="disabled human H1 RNA promoter"
1991. .2122
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/note="Cytb-AS; partial human cytochrome
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/gene="Amp"
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                                                                                  AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
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/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_xrefs"ttaxon:32630"
/noTe="fusion construct homo sa
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sequences; artificial sequences
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/mal_type="taxon:32630"
/mbe="pla710"
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synthetic construct
other sequences; artificial sequences.
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           (1-225)
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Patent: WO 2005012534-A 23 10-FEB-2005;
Oxitec Limited (GB)
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5327 100 5267 5207 60 5147 40 5087

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                     CACCACCTGTTCCTG 8212
                                                                        IleThrSerHisAsnGluAspTyrThrIleValGluGinTyrGluArgThrGluGlyArg
                                                                                                                                              ACCCACAAGGCCCTGAAGCTGAAGGACGGCCGCCACTACCTGGTGGAGTTCAAGTCCATC
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                                                             ATCACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGC
                                                                                                                 TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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/mal_type="unassigned DNA"
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/noTe="pLA517"
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/mote="pLA1188"
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                                                                        LygValLygPheIleGlyValAgnPheProSerAgpGlyProValMetGlnLygLygThr 140
                                                                                                                  AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                              GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG 8252
                                                                                                                                                         AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                                                                                                       CTGTCCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC 8192
IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="unassigned
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/note="pLA513"
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US-10-006-922A-12 (1-225) x CS018257 (1-14720)
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                                                     AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="pLA1038"
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RESULT 52
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Patent: WO 2005003364-A 3 13-JAN-2005;
Oxitec Limited (GB)
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                                               LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80
                                                                                                                                            ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCCCTACGAGGGCC
                                                                                                                                                           ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                                                                                                                                    ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
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 AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                    CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATC
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Stable integrands
Patent: WO 2005003364-A 4 13-JAN-2005;
Oxitec Limited (GB)

Location/Qualifiers

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                                                                                                   1 MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly
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                                                                                    ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
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                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                    note="predicted sequence of pLA1125 construct"
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          US-10-006-922A-12
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Sequence 11
AX686888
AX686888.1
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
Corallimorpharia; Discosomatidae; Discosoma.
                                                                                                                                                                                                      Patent: WO 0127150-A 11 19-APR-2001;
Clontech Laboratories Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         Discosoma sp.
                                                                                                                                                                                                                                                           Lukyanov, S.A., Fradkov, A.F., Labas, Y.A.,
Anthozoa derived chromo/fluoroproteins a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leu8erProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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          (1-225)
                                                                                                                                                  /organism="Discosoma sp."
/mol_type="unassigned DNA'
/db_xref="taxon:86600"
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Choe, J., Guo, H.H. and van den Engh, G.
A dual-fluorescence reporter system for high-throughput characterization and selection by cell sorting (er) Nucleic Acids Res. 33 (5), E49 (2005)
                                                                                                                                                                                                Dual fluorescent protein cloning vector pGRFP Dual fluorescent protein cloning vector pGRFP other sequences; artificial sequences; vectors
                                                                                                                                                                                                                                                   AY916793
Dual fluorescent protein cloning
AY916793
AY916793.1 GI:60101687
                                      Submitted (01-FEB-2005) Laboratory of Ger van
for Systems Biology, 1441 N 34th St, Seattle,
Location/Qualifiers
                                                                            2 (bases 1 to 3441)
Choe, J., Guo, H.H. and van den Engh, G.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                             HisHisLeuPheLeu 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Dual fluorescent
/mol_type="other DNA"
                              .3441
                                                                                                                                                                                                                                                                               vector pGRFP, complete
                                                                                                                                                                                                                                                                                            DNA
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                                            HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                                                                                                                                                                                                                                                                    MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="GRFP"
/gene="GRFP"
/note="faster folding mutant of discosoma red fluorescent
/note="faster folding mutant of discosoma red fluorescent
protein; derived from pDsRed-T3; silent mutations have
been introduced to change restriction sites; Region:
discosoma red fluorescent protein T3 mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="GRFP"
/note="contains G,S residues for flexibility on each side,
/note="contains G,S residues for flexibility on each side,
M13 forward and reverse primer sites, and NotI, EcoRV,
Sall cloning sites, Region: linker"
953. .1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="cycle 3 mutant of GFP; derived initially from pGFPmut3.1; Region: green fluorescent protein mutant 3.1" 854. .952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/trans_table=11
/product="beta-lactamase"
/protein_id="AAX13968.1"
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/grotein_id="AAX13968.1"
/db_xref="G:60101688"
/trans1stion="MSIOHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDOLGARVGY
/tra
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KFICTTGKLPVBPTLVTTFGYGVQCFARYDDHXQHDFFKSAMPEGYVQERTIFFKD
DGNYKTRAEVKEEGDTLVNTEKSGIDFKEDGNILGHKLEXYNVNSHVVYIMADKÇNG
IKVNFKIRHNIEDGSVQLADHYQQNTFIGDGPVLLPDNHYLSTQSALSKDPNEKRDHM
VLLEFYTAAGITHGMDELYKSGSGSGCKTTASSAAADISVDGHSCFTAGSGSGSASSE
DVIKEFMFFKVRMEGSVNGHEFEIEGEGEGFRPYEGTQTAKLKVTKGGPLPFAMDILSF
QFQYGSKVYVKHPADIFDYKKLSFPEGEFKMERVMNFEDGGVVTVTQDSSLQDGCFIYK
VKFIGVNFPSDGPVNQKKTNGMEPSTERLYPRDGVLKGEIHKALKLDGGHYLVEFKS
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with an intervening linker region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:314306" 140. .1630
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/protein_id="AAX13969.1"
/db_xref="GI:60101689"
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/transl_table=11
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Cloning v
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Location/Qualifiers
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                                                                                                                                                                                                                                                       organism="Cloning vector"
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                       gene for Ds Red fluorescent
AJ851289
AJ851289.1 GI:55724885
beta-glucuronidase; Ds Red
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                                                                                                                                                                       HisHisLeuPheLeu
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                                                                                                                                                                                                                                                                     TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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                                                                                                                                             CACCACCTGTTCCTG
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IHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTE
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Submitted (21-OCT-2004) Poole P.S., School of AMS, University
Reading, Whiteknights, Reading, RG6 6AJ, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning vector pRU1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karunakaran, R. and Poole, P.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          high throughput promoter
HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                                                                                     ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
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TLAGLHSMYTDMWSEEYQCARLDMYHRVFDBVSAVVGEQVMNFADFATSQGILRVGGN
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885. .2696
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/mol_type="other DNA"

/db_xref="taxon:299184"
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Cloning vector pRUI1166
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                                                                                                                                  Direct Submission
Submitted (21-OCT-2004) Poole P.S.,
Reading, Whiteknights, Reading, RG6
Location/Qualifiers
                                                                                                                                                                                              High throughput
Unpublished
                                                                                                                                                                                                                                                                                                      AJ851286
Cloning vector pRU1106
                                                                                                                                                                            Poole, P.S.
                                                                                                                                                                                                                  Karunakaran, R. and Poole, P.
                                                                                                                                                                                                                                                                                                                                                                      HisHisLeuPheLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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                                                                                                                                                                                                                                     sequences; artificial sequences;
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)26. .1003
                                                                                   /lab_host="Escherichia coli"
                                                                                               organism="Cloning vector/mol_type="other DNA"

/db_xref="taxon:299181"
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AY342347.1 GI
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                                                                                        CACCACCTGTTCCTG
   H-Pelican DsRed.T4 transformation
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/translation="massedvikefwrfkvrmegsvnghefiegegegrpyegtqta klkvtkgeflefawdiispofoygskvyvkhfadiedykklsfpegffwervmffedg gvvtvtogosslodgcfiykvffigvnfpsdgpvmqkktmgmepsterlyfrdgvikge ihkalklkdgghylvefksiymakkevqlpgyyyvdsklditshnedytiveqyfrae grhhlfl"

1.74e-108 1165.00 97.33% 96.00% 95,96% 11 Mismatches: Indels: Conservative:

Gaps:

5311 216 3 6 0

21 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle | IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC ATGGGCTGGGAGCCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCCGAG MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu |||||||||| **AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCCGTAATGCAGAAGAAGACT** LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr GACGGCGGCGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG CTGTCCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro ACCCAGACCGCCAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATC TCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCCGAGGGCCCCCTACGAGGGC ATGGCCTCCTCCGAGGACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly racaccategrageageagtaegagegeegeegaggeeeee (1-5311) 200 180 120 60 385 925 865 805 160 745 140 685 625 100 565 80 505 445 40 20 985

GI:33358309

vector

DsRed.T4 transformation

vector,

linear complete

SYN 21-OCT-2003 sequence.

10141

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21-OCT-2003

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Direct Submission
Submitted (14-JUL-2003) Division of Biology/CDB,
Submitted (14-JUL-2003) Division of Biology/CDB,
Hall, MC 0349, La Jolla, CA 92093-0349, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Red H-Pelican DsRed.T4 transformation vector other sequences; artificial sequences; vectors.

1 (bases 1 to 1014)
Barolo,S. and Posakony,J.W.
Advances in Drosophila Transgenic Reporters I: Fast-Maturing RFP [DsRed.T4] and Nuclear RFP in Insulated Vectors
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Barolo, S. and Posakony, J.W.
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                                                                                       TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
                                                                                                                                                     IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                              ATGGGCTGGGAGCCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
                                                                                                                                                                                                              | MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                                                                         AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACT
                                                                                                                                                                                                                                                                                                                                         AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
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                                  IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                       TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC
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Submitted (14-JUL-2003) Division of Biology/CDB,
Hall, MC 0349, La Jolla, CA 92093-0349, USA
Location/Qualifiers
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Red H-Stinger DsRed.T4-NLS transformation vector
other sequences; artificial sequences; vectors.
1 (bases 1 to 10276)
Barolo,S. and Posakony,J.W.
Advances in Drosophila Transgenic Reporters I: Fast-Maturing RFP
[DsRed.T4] and Nuclear RFP in Insulated Vectors
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AY342348
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                                                                                                                                                                                                                                                                                                                                                                                                                  MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
TCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGC
                                                                                                                                                                                                                                                                                                                                                                     ThrvalAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                                                           AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                                                                                                                CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
                                                                                                                                                                                                                                                LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80
                                                                                                                                                                                                                                                                                          ACCCAGACCGCCAAGCTGAAGGTGACCAAGGGCGGCCCCTGCCCTTCGCCTGGGACATC
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                                                            LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
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/db_xref="taxon:240545"
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Direct Submission
Submitted (13-NOV-2003) Cell & Developmental Biology, Univers
Michigan Medical School, 5732 Med Sci 2, Ann Arbor, MI 48109,
Location/Qualifiers
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Barolo,S. and Posakony,J.W.
Advances in Drosophila Tran
[DsRed.T4] and Nuclear RFP
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/mol_type="other DNA"
/db_xref="taxon:258595"
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Cloning vector pRU1076
Cloning vector pRU1076
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beta-glucuronidase; Ds |
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/Codon_start=1
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GVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEPSTERLYPRDGVLKGE
                                                                                                                                                                      /organism="Cloning vector
/mol type="other DNA"
/db xref="taxon:299185"
/lab host="Escherichia col
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                                                                                                                    gene="dsRedT4"
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                                                                                       IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                                                                                                                            MetGlYTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                           AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACT
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                           TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp 200
                                                                                                                                        ATGGGCTGGGAGCCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
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/transl_table=11
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Percent Similarity:
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AF506025
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A monomeric red fluorescent protein
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 7877-7882 (2002)
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Campbell, R.E. and Tsien, R.Y.
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                                                                                                               ThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSer 62
                                                  AsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsn 42
                                                                                            TCCTCCGAGGACGTCATCAAAGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCTCCGTG
                                AACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCCCTACGAGGGCACCCAG 129
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AKLKVTKGGPLPFAMDILSPQFQYGSKAYVKHPADIPDYKKLSFPEGFKWERVMNFED
GGVVTVTQDSSLQDGTLIXKVKFRGTNFPFDGPVMQKKTMGWEASTERLYPRDGVLKG
BIHQALKLKDGGHYLVEFKTIYMAKKPVQLFGYYYVDTKLDITSHNEDYTIVEQYERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="dimer2; engineered variant of tetrameric fluorescent protein from Discosoma deposited in Accession Number AAF03369"
                                                                                                                                                                                                                                                                                                                                                                                               /producT="dimeric red fluorescent protein"
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/db_xref="taxon:32630"
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other sequences, artificial sequences.

1 (bases 1 to 1395)
1 (bases 1 to 1395)
1 Campbell,R.E., Tour,O., Palmer,A.E., Steinbach,P.A., Baird,G.S.,
Cacharias,D.A. and Teien,R.Y.
A monomeric red fluorescent protein
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 7877-7882 (2002)
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Campbell, R.E. and Tsien, R.Y.
Direct Submission
Submitted (24-Apr-2002) Pharmacology,
Jolla, CA 92093, USA
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/db xref="taxon:32630"
/noTe="from Discosoma sp.; Clontech vector
human optimized codon usage"
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DGVLKGEIHQALKLKDGGHYLVEFKTIYMAKKPVQLPGYYYVDTKLDITSHNEDYTIV
EQYERSEGRHHLFL"
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red. No.: core: core: bercent Similarit lest Local Simila puery Match:	red. No.: 1.06e-104 Length: 1395 core: 1121.00 Matches: 207 ercent Similarity: 95.96% Conservative: 7 est Local Similarity: 92.83% Mismatches: 9 puery Match: 92.34% Indels: 0 B: Gaps: 0
18-10-006-9	922A-12 (1-225) x AF506026 (1-1395)
ਲੋਂ ਝੋਂ	3 SerSerLysAsnVallleLysGlupheMetArgPheLysValArgMetGluGlyThrVal 22
ਲੋਂ 'ਝੋਂ	23 AsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsn 42 
¥	43 ThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSer 62
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ř	190 CCCCAGTTCCAGTACGGCTCCAAGGCGTACGTGAAGCACCCCGCCGACATCCCCGACTAC 249
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<del>ن</del> 2	50 AAGAAGCTGTCCTTCCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGC 309
7 1	103 GlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysVal 122
ъ 3	310 GGCGTGGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCACGCTGATCTACAAGGTG 369
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ъ 3	370 AAGTTCCGCGGCACCAACTTCCCCCCCGACGGCCCCGTAATGCAGAAGAAGACCATGGGC 429
T A	143 TrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHis 162
<del>ن</del>	430 TGGGAGGCCTCCACCGAGGCCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAGATCCAC 489
Į.	163 LysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIleTyrMet 182
<del>δ</del>	490 CAGGCCCTGAAGGTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGACCATCTACATG 549
נ ענ	183 AlaLysLysProValGlnLeuProGlyTyrTyrTyrTvalAspSerLysLeuAspIleThr 202
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<i>y</i> 2	03 SerHigAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArgHisHis 222
ğ. Θ	10 TCCCACAACGAGGACTACACCATCGTGGAACAGTACGAGCGCTCCGAGGGCCGCCACCAC 669
<i>y</i> 2	23 LeuPheLeu 225
6	70 CTGTTCCTG 678

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AX824729.1 GI:39750593
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other sequences; artificial sequences.
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                                                                                                                                                      MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                           LysVallysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                                                                                                                                                                                                            AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAGCTGCAGCAAGAACGTGATCAAGGAGTTCATGCGGTTCAAGGTGCGGATGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetArgSerSerLy8AsnVallleLy8GluPheMetArgPheLy8ValArgMetGluGly
                                                                                 ATCCACATGGCCCTCCGGCTCGAGGGCGGCGCCACTACCTCGTGGAGTTCAAGAGCATC
                                                                                               IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                                                                                                     CGGGGCTGGGAGGCCAGCAGCGAGCGGCTCTACCCCCGGGACGGCGTGCTCAAGGGCGAC 480
                                                                                                                                                                                         GAGGTGAAGTTCATCGGCGTGAACTTCCCCCAGCGACGGCCCCGTGATGCAGCGGCGGACC
                                                                                                                                                                                                                                                GACGGCGGCGTGATCATCTAC
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                                                                                                                                                                                                                                                                                                                      AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                                                                                                                                                                                                                                                                          CTCAGCCCCAGTTCCAGTACGCCAGCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
 IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg 220
                                            TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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/mol_type="unassigned DNA"
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Submitted (06-JUL-2004) Pharm
Diego, 9500 Gilman Dr., La Jo
Location/Qualifiers
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Improved monomeric red, orange and yellow fluorescent proteins derived from Discosoma sp. red fluorescent protein Nat. Biotechnol. 22 (12), 1567-1572 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shaner, N.C., Campbell, R.E., Steinbach, P.A.,
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                                                                  HisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsnThrVal 44
                                                                                                                                    LysAsnValIleLysGluPheMetArgPheLysValArgMetGluGlyThrValAsnGly
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EIHQALKLKUGGHYLVEFKTIYMAKKPVQLPGYYYVDTKLDITSHNEDYTIVEQYERS
EGRHHLFLYGMDELYK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="dTomato; engineered variant of dimeric red fluorescent protein dimer2 in GenBank Accession Num AF566025; N- and C-termini replaced with equivalent
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construct dimeric red fluorescent protein gene, complete
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La Jolla, CA 92093-0647,
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                                                                                                                                                                                                                                                        other sequence, [1]

1 (bases 1 to 1431)
Shaner,N.C., Campbell,R.E., Steinbach,P.A., Giepmans,B.N.,
Palmer,A.E. and Tsien,R.Y.
Improved monomeric red, orange and yellow fluorescent proteins
derived from Discosoma sp. red fluorescent protein
derived from Discosoma sp. red fluorescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                      AY678269 1431 bp DNA linear Synthetic construct tandem-dimer red fluorescent p complete cds.
AY678269 AY678269.1 GI:55420622
                                                                                                                                                                     Submitted (06-JUL-2004) Pharmacology, University of California, Diego, 9500 Gilman Dr., La Jolla, CA 92093-0647, USA
                                                                                                                                                                                                                                                                                                                                                                        synthetic construct other sequences, artificial sequences.
                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                Shaner, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                          synthetic
                                                                                                                                                                                                                        Tsien, R.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAspIleThrSerHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHisLysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGACCGTGACCCAGGACTCCTCCCTGCAGGACGCCACGCTGATCTACAAGGTGAAGATG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGlyGlyVal 104
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ner, N.C., Campbell, R.E.,
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                /note="tdTomato; engineered variant of dimeric red
fluorescent protein dimer2 in GenBank Accession Number
AF506025, N- and C-termini replaced with equivalent
residues from EGFP"
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                                                                                                                                                                                                                                                                                                                                                                                            construct
                                                                                                                                                        location/Qualifiers
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                                                                                                                                                                                                                                   Steinbach, P.A.,
                                                                                                                                                                                                                                     Palmer, A.E.
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GGLVTVTQDSSLQDGTLIYKVKNGFGTNFPDGPVMQKKTMGWEASTERLYPRDGVLKG
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LYPRDGYLKGEHLQALKHKDGGHYLVEFKTIYMAKKPVQLPGYYYVDTKLDITSHNED
YTIVEQYERSEGRHHLFLYGMDELYK"
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Pred. No.:	
Score: Percent Similarity: Best Local Similarity: Ouery Match:	1095.00 Matches: 94.57% Conservative: 90.95% Mismatches: 90.20% Indels:
DB:	Gарв:
US-10-006-922A-12 (1-	2A-12 (1-225) x AY678269 (1-1431)
Qy 5 Db 16	<pre>5 LysAsnVallleLysGluPheMetArgPheLysValArgMetGluGlyThrValAsnGly 24 5::-   </pre>
Оу 25	HisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsnThrVal 44
Db 76	
Qy 45	
Db 136	AAGCTGAAGGTGACCAAGGGCGCCCCCTGCCCTTCGCCTTGGGACATCCTGTCCCCCCAG 195
Ωγ 65	
Db 196	TTCATGTACGGCTCCAAGGCGTACGTGAAGCACCCCGCCGACATCCCCGATTACAAGAAG 255
Оу 85	LeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGlyGlyVal 104
Db 256	
Qу 105	ValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysValLysPhe 124
Db 316	
Оу 125	IleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGlyTrpGlu 144
Db 376	
Qy 145	AlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHisLysAla 164
Db 436	
Qу 165	
Db 496	
0у 185	
Db 556	
Qy 205	
Db 616	AACGAGGACTACATCGTGGAACAGTACGAGCGCTCCGAGGGCCGCCACCACCACCTGTTC 675
Оу 225	
Db 676	CTG 678

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VERSION
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AF272711
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Discosoma sp. SSAL-2000
Discosoma sp. SSAL-2000
Eukaryota, Metazoa, Chidaria, Anthozoa, Zoantharia,
Eukaryota, Metazoa, Chidaria, Anthozoa, Zoantharia,
Corallimorpharia, Discosomatidae, Discosoma.

Corallimorpharia, Discosomatidae, Discosoma.

Corallimorpharia, Discosomatidae, Discosoma.

Corallimorpharia, Discosomatidae, Discosoma.
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AF272711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-MAY-2000) Institute of Bioorganic Miklukho-Maklaya 16/10, Moscow 117871, Russia
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Lukyanov, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        possesses a unique far-red fluorescence
FEBS Lett. 479 (3), 127-130 (2000)
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Lukyanov,S.A.
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                                                                                                                                                                                                              MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly
                                                                                                           H18A8nThrValLy8LeuLy8ValThrLy8GlyGlyProLeuProPheAlaTrpAspIle
                                                                                                                                                                        ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                         CACTGTTCCGTAAAGCTTATGGTAACCAAGGGTGGACCTTTGCCATTTGCTTTTGATATT
                                                                                                                                                     ACGGTCAATGGGCACGAGTTTGAAATAAAAGGCGAAGGTGAAGGGAAGGCCTTACGAAGGT
                                                LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mscsknvikefmrfkvrmegtvngheflikgegegrpyeghcsvkmvtkggplpfafdilspqfqygskvyvkhfadipdykklsfpegfkwervmfedggvvtvsqdsslklyfrdgvlfgdgrvrqpsdgpvmqrrtrgweasserlyfrdgvlkgdihmalrleggghyvvektyvkfbyqlpgyyydskldmtshnedytvveqyekt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="FP593"
45. .737
                                                                                                                                                                                                                                                                                                                                                                                                                                            OGRHHPFIKPLO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="FP593"
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95.58%
88.05%
89.42%
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
Eukaryota; Metazoa; Discosomatidae; Discosoma.
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AX686894
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                                                                                                                                                                                                                                                                        Patent: WO 0127150-A 17 19-APR-2001; Clontech Laboratories Inc. (US)
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                                                        MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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                                                                                                              Submitted (24-APR-2002) Pharmacology, Jolla, CA 92093, USA
                                                                                                                                                                         Campbell, R.E., Tour, O., Palmer, A.E., St
Zacharias, D.A. and Tsien, R.Y.
A monomeric red fluorescent protein
Proc. Natl. Acad. Sci. U.S.A. 99 (12),
                                                                                                                                                                                                                           synthetic construct other sequences.
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Campbell, R.E. and Tsien, R.Y.
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                                                                                                                                                                                           MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
                                                                          LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                             TCTGTTAATGGACATGAGTTCGAGATTGAGGGGGAAGGAGGGGAAGACCTTACGAGGGG
                 AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                    ACTCAGACTGCTAAGCTGAAGGTTACTAAGGGGGGACCACTGCCTTTCGCTTGGGATATC
 GACTATTTGAAGCTCTCTTTCCCAGAAGGATTCAAGTGGGAGAGAGTTATGAACTTCGAG
                                                          CTGTCTCCACAATTCCAATACGGATCTAAGGCTTACGTCAAGCATCCAGCAGATATCCCA
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nt protein, partial cds.
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/note="Synthetic monomeric DsRe
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                            Chung, S.-M., Vyas, S., Kozlovskiy, S., Citovsky, V. and Tz Direct Submission Submitted (12-APR-2005) Department of Biochemistry and Biology, State University of New York at Stony Brook, S NY 11794, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chung, S.-M., Vyas, S. and Tzfira, T. A versatile vector system for mult unpublished
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1 (bases 1 to 4543)
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                                                                                                IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg 220
                                                                                                                                       TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAAGACCGACATCAAGCTGGAC
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YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFKELTAFLHNMGDHVTRL
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/note="CaMV 35S terminator"
complement(3483. .4343)
/note="amp resistance"
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LRSALPAGWFI ADKSGAGERGSRGI I AALGPDGKPSRI VVI YTTGSQATMDERNRQI A
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/product="Bla"
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DQ005474
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US-10-006-922A-12 (1-225) x DQ005474 (1-4555)
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Submitted (12-APR-2005) Department of Biochemistry and Cell
Biology, State University of New York at Stony Brook, Stony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other sequences; artificial sequen 1 (bases 1 to 4555) Chung, S.-M., Vyas, S. and Tzfira, T.
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Cloning vector pSAT6-RFP-C1,
D0005474
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                                                                                                                                                                        /protein_id="AAY25383.1"
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DRWEFPELNEAIFNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDMMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGFDGKPSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW"
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/product="RFP"
/protein_id="AAY25382.1"
/db_xref="GI:63002547"
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441. .762
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mol_type="other DNA"
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                                                                                                                     Submitted (12-APR-2005) Department of Biochemistry and Cell Biology, State University of New York at Stony Brook, Stony Brook, NY 11794, USA
                                                                                                                                                                                                                                           1 (bases 1 to 4558)
Chung, S.-M., Vyas, S. and Tzfira, T.
A versatile vector system for multiple gene expression
                                                                                                                                                                         2 (bases 1 to 4558)
Chung, S.-M., Vyas, S.,
Direct Submission
                                                                                                                                                                                                                                                                                                                    Cloning vector pSAT6-RFP-N1
Cloning vector pSAT6-RFP-N1
                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                     other sequences; artificial
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/note="CaMV 35S
                                                                                                    Location/Qualifiers
                                                                                                                                                                                          Kozlovskiy, S., Citovsky, V. and Tzfira,
                                                                                                                                                                                                                                                                                                                                                                                                                                4558
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                                                                                                                                                                                                                                                                                                                                                                      HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGCCTCCTCCGAGGACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
                                                                                       LysvalLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                                           GACGGCGGCGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTAC
                                                                                                                                                            AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
                                                                                                                                                                                                    GACTACTTGAAGCTGTCCTTCCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                                                                                                      AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                                                                                                                                                                                         CTGTCCCCTCAGTTCCAGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCC
                                                                                                                                                                                                                                                                                               LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY IELDLNSGKILESFRPEERFPWMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFKELTAFLHNMGDHVTRL DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLDWBEADKVAGPLLEASALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAY25384.1"
/db_xref="qI:63002550"
/translation="MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTA
/translation="MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTA
/translation="MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEKWERVMNFEDG
KLKYTKGGFLPFAWDIKLTGTNFPSDGPVMQKKTMGWEASTERMYPEDGALKGE
GVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASTERMYPEDGALKGE
IKMRLKLKDGGHYDAEVKTTYMAKKFVQLPGAYKTDIKLDITSHNEDYTIVEQYERAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="CAMV 35S promoter"
1190. .1320
/note="translational enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="CaMV 35S terminator" complement (3498. .4358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1395
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/db_xref="GI:63002551"
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84.10%
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Matches:
Conservative:
Mismatches:
Indels:
                                                               CGGCCCCGTAATGCAGAAGAAGACC
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AJ851287
LOCUS
                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                          US-10-006-922A-12 (1-225) x AJ851287
                                                                                                                                                               Alignment Scores:
Pred. No.:
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    326
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Reading, Whiteknights, Reading, RG6
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mono Red fluorescent particle (Cloning vector pRU1144 Cloning vector pRU1144
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Cloning vector pRU1144 mRFP1
AJ851287 GI:55724880
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Karunakaran, R. and Poole, P.
High throughput promoter po
MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 5311)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences; artificial sequences;
                                                                                                                                                                                                                                    /translation="massedvikefmrekvrmegsvnghefeiegeggrpyegtqtakkkvykggplpfawdilspqfqygskayvkhpadipdylklsppegfkwervmnfedg
Klkvtkggplpfawdilspqfqygskayvkhpadipdylklsppegfkwervmnfedg
Gvvtvtqdsslqdgefiykvklrgtnfpsdgpvmqkktmgweastermypedgalkge
Ikmrlklkdgghydaevktttymakkpvqlpgayktdiklditshnedytiveqyerae
                                                                                                                                                                                                                                                                                           /gene="mRFP1"
/codon_start=1
/transI_table=1
/transI_table=1
/product="mono_Red_fluorescent_protein"
/protein_id="CAH64892.1"
/db_xref="GI:55724881"
                                                                                                                                                                                                                                                                                                                                                                                     /gene="mRFP1"
126. .1003
                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Cloning vector pRU1144"

mol_type="other DNA"
                                                                                       8.78e-94
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Matches:
Conservative:
Mismatches:
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gene
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KEYWORDS
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AJ851291
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                                                                                  Direct Submission
Direct Submission
Submitted (21-OCT-2004) Poole P.S.,
Reading, Whiteknights, Reading, RG6
Location/Qualifiers
                                                                                                                                                                                                                                                                                            AJ851291 13079 bp DNA circular SYN Cloning vector pRU1161 gusA gene for beta-glucuronidase gene for mono Red fluorescent protein.
AJ851291 AJ851291.1 GI:55724891 beta-glucuronidase; gusA gene; mono Red fluorescent prot
                                                                                                                                                                                             High
                                                                                                                                                                                                                                                    Cloning vector pRU1161
Cloning vector pRU1161
                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                    Poole, P.S.
                                                                                                                                                                              Unpublished
                                                                                                                                                                                                             Karunakaran, R. and Poole, P.
                                                                                                                                                                                                                                          other sequences; artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                              His
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 /organism="Cloning vector pRU:
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                                                                                            AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                             GACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                                                                CTGTCCCCTCAGTTCCAGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCC
                                                                                                                                                                                                                                 ACCCAGACCGCCAAGCTGAAGGTGACCAAGGGCGCCCCCTGCCCTTCGCCTGGGACATC
MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                             GACGGCGGCGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTAC
                                          LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
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IKMRLKLKDGGHYDAEVKTTYMAKKPVQLPGAYKTDIKLDITSHNEDYTIVEQYERAE
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885. .2696
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/transI_table=11
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US-10-006-922A-12 (1-225) x AY678271 (1-678)
                                          Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other sequences; artificial sequences.
1 (bases 1 to 678)
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                                                                                                                                                                                            /translation="massedvikefmrfkvrmegsvnghefeiegeggrpyegtQtakkvrkggplpfamdilspqfmmgskayvkhpadipdylklsppegfkmervmnfedggvytytyddsslodgefiykvklrgtnfpsddpvmgkktmgmaattermypedgalkge
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                                                                                                                                                                                                                                                                                                                                note="mHoneydew; engineered variant of monomeric red
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Direct Submission
Submitted (06-JUL-2004)
Diego, 9500 Gilman Dr.,
                                                                                                                  Shaner, N.C., Campbell, R.E., Steinbach, P.A., Giepmans, F. Palmer, A.E. and Tsien, R.Y.
Improved monomeric red, orange and yellow fluorescent derived from Discosoma sp. red fluorescent protein that. Biotechnol. 22 (12), 1567-1572 (2004)
                                                                                                                                                                                                      synthetic construct other sequences; artificial sequences 1 (bases 1 to 678)
                                                    Tsien, R.Y.
                                                                 Shaner, N.C.,
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 Pharmacology, University La Jolla, CA 92093-0647,
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                                                      TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAAGACCGACATCAAGCTGGAC
                                                                                                                       ATCAAGATGAGGCTGAAGGTGAAGGACGGCGGCCACTACGACGCCGAGGTCAAGACCACC
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KUNTTQDSSLQDGEFIYKVKLRGTNFFSDGPVMQKKTMGWEASSERMYFEDGALKGE
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/db_xref="taxon:32630"
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Submitted (07-JUL-2004) Chemistry,
Lichtenbergstr. 4, Garching 85747,
Location/Qualifiers
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A brilliant monomeric red fluorescent protein to visualize Cytoskeleton dynamics in Dictyostelium FEBS Lett. 577 (1-2), 227-232 (2004)
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        ACACAAACAGCAAAATTAAAAGTTACAAAAGGTGGTCCATTACCATTTGCATGGGATATT
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682. .699
/note="Region: histidine-tag; 6xHis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 711)
Shaner, N.C., Campbell, R.E.
Palmer, A.E. and Tsien, R.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete cds.
AY678265
                                                                                                                                                                                                                                                 Submitted (06-JUL-2004) Pharmacology, University Diego, 9500 Gilman Dr., La Jolla, CA 92093-0647, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 711)
Shaner, N.C., Campbell, R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Improved monomeric red, orange and yellow fluorescent derived from Discosoma sp. red fluorescent protein Nat. Biotechnol. 22 (12), 1567-1572 (2004)
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                                                                                                                                                                                                                                                                                                                                      Tsien, R.Y
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                                                        /note="mOrange; engineered variant of monomeric red fluorescent protein mRFP1 in GenBank Accession Number AF506027; N- and C-termini replaced with equivalent residues from EGFP"
                                                                                                                                                                                     organism="synthetic construct"
/mol_type="other DNA"
                     /codon_start=1
/transl_table=
                                                                                                                                                                  /db_xref="taxon:32630"
/product="monomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campbell, R.E., Steinbach, P.A., Giepmans, B.N.,
                   _table=11
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  orange fluorescent protein"
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92093-0647, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAV52165.1"
/db_xref="G1:55420615.1"
/db_xref="G1:55420615."
/db_xref="G1:55420615."
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GFQTAKLKVTKGGPLPFAWDILSPQFTYGSKAYVKHPADIPDYFKLSFPEGFKWERVM
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ALKGEIKMRLKDGGHYTSEVKTTYKAKKPPQLPGAYIVGIKLDITSHNEDYTIVEQ
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Improved monomeric red, orange and yellow fluorescent derived from Discosoma sp. red fluorescent protein Nat. Biotechnol. 22 (12), 1567-1572 (2004)
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Location/Qualifiers
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1 (bases 1 to 711)
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                 ValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGlyTrpGluAlaSer
                                                         GTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGC 393
                                                                              ValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysValLysPheIleGly 126
                                                                                                                                      PheProGluGlyPheLy8TrpGluArgValMetAsnPheGluAspGlyGlyValValThr 106
                                                                                                                                                                                                  TyrGlySerLysValTyrValLysHisProAlaAspIleProAbspTyrLysLysLeuSer 86
                                                                                                                                                                                                                                                AAGGTGACCAAGGGTGGCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATG
                                                                                                                                                                                                                                                                  LysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSerProGlnPheGln
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aner, N.C., Campbell, R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl table=11
/product="monomeric red f:
/protein id="AAV52164.1"
/db_xref="gI:55420613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGGRPYE
GTQTAKLKVTKGGFLÞFAMDILSPQFMYGSKAIVKHPADIPDYLKLSFPEGFKMERVM
NFEDGGVVTVDDSSLQDGEFIYKVKLRGTNFFSDGFVMQKKTMGWEASSERMYFEDG
ALKGEIKQRLKLDGGHYDAEVKTTYXAKKFVQLÞGAYNVNIKLDITSHNEDYTIVEQ
YERAEGRHSTGGMDELYK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="mCherry; engineered variant of monomeric red fluorescent protein mRFP1 in GenBank Accession Number AF506027; N- and C-termini replaced with equivalent residues from EGFP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/mol type="other DNA"
/db xref="taxon:32630"
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Discosoma
25 H1sGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsnThrVal
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Direct Submission
Submitted (18-OCT-2004) Department of Pharmacology, University of
California-San Diego, 9500 Gilman Drive, La Jolla, CA 92093, USA
Location/Qualifiers
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Discosoma sp. LW-2004
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Corallimorpharia; Discosomatidae; Discosoma.
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                                             GTGCAGCTGCCCGGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAG
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                                                                                                                                                                                                                                                                                                    /translation="myskgeevikefmrfkvrmegsvnghefelegeggrpyegtqt
aklkvtkggplpfamdilspqcmygskgyvkhpadipdylklsfpegfkwervnnfed
ggvvtvtqdsslqdgefiykvklrgtnfpsdgpvmqkktmgweassermypedgalkg
                                                                                                                                                                                                                                                                                                                                               /codon start=1
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/protein id="AAV65486.1"
/db_xref="G1:55792807"
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xref="taxon:301246"
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1 (bases 1 to 711)

1 (bases 1 to 711)

Shaner,N.C., Campbell,R.B., Steinbach,P.A., Giepmans,B Palmer,A.E. and Tsien,R.Y.

Improved monomeric red, orange and yellow fluorescent derived from Discosoma sp. red fluorescent protein Mat. Biotechnol. 22 (12), 1567-1572 (2004)
                                                                                                                                                       Submitted (06-JUL-2004) Pharmacology, University of California, Diego, 9500 Gilman Dr., La Jolla, CA 92093-0647, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCATGTACGGCTCCAAGGGCTACGTGAAGCACCCCGGCGACATCCCCGACTACTTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACGAGGACTACACCATCGTGGAACAGTACGAGCGCGCCGAGGGCCGCCAC
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                                                                                                                                                                                                                                  (bases 1 to 711)
ner,N.C., Campbell,R.E.,
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                                                                                                                                                            GACTACACCATCGTGGAACTGTACGAACGCGCCGAGGGCCGCCAC
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                                                                                                                                                                                AspTyrThrIleValGluGlnTyrGluArgThrGluGlyArgHis 221
                                                                                                                                                                                                                                GTGCAGCTGCCCGGCGCCTACATCGTCGGCATCAAGTTGGACATCACCTCCCACAACGAG
                                                                                                                                                                                                                                                    ValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAspIleThrSerHisAsnGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysValLysPheIleGly 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGlyGlyValValThr 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALKGEIKMRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYIVGIKLDITSHNEDYTIVEL
YERAEGRHSTGGMDELYK"
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
Corallimorpharia; Discosomatidae; Discosoma.
1 (bases 1 to 681)
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                  IleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGlyTrpGlu
                                                                                                                                                                                ValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysValLysPhe 124
                                                                                                                                                                                                                                CTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTG
                                                                                                                                                                                                                                                    LeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGlyGlyVal
                                                                                                                                                                                                                                                                                                      ATCATGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCCGACTACTTGAAG
                                                                                                                                                                                                                                                                                                                                                                          AGGCTGAAGGTGACCAAGGGTGGCCCCCCGCCCTTCGCCTGGGACATCCTGTCCCCCTCAG
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                                                                                                                                                            GTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGGTG
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University of CA 92093, USA

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VERSION KEYWORDS SOURCE

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165 LeutysLeutysAspGlyGlyHisTyricsUvalGlubhelysSerTleTyrMethlalys 184 496 [[Hi]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]	Alignment & Pred. No.: Score: Percent Sin Best Local Query Matcl DB:  US-10-006-Oy  Oy  Oy  Oy	ORIGIN	cos	REFERENCE AUTHORS TITLE JOURNAL FEATURES	YWORDS URCE ORGANIS FERENCE AUTHORS AUTTLE JOURNAL PUBMED	RESULT 85 AY678267 LOCUS DEFINITION ACCESSION	B & B &	
	1.28e-88	Illusrescent protein mkrf1 in Geneaux Accession Number AF506027, N and C-termini replaced with equivalent residues from EGFP"  /codon start=1  /transI_table=11  /prodein=monomeric yellow-orange fluorescent protein" /protein_id="AAV52167.1"  /db_xref="GI:55420621"  /db_xref="GI:55420621"  /translation="MVSKGENNWAVIKEFWRFKVRMEGSVNGHEFEIEGEGEGRPYE /translation="MVSKGENNYAVIKEFWRPFSDGPVMGKTMGWEASSERMYEDG GTQTAKLKVTKGGPLFPAMDILSPQFCYGSKAYVKHPTGIPDYFKLSFPEGFKWERVM GFEDGGVVTVAQDSSLQDGEFIKKVKLKGFWPPSDGPVMGKKTMGWEASSERMYPEDG ALKGEIKMELKLUOGGHYGAETKTTYKAKKPVQLPGAYIAGEKIDITSHNEDYTIVEL YERAEGRHSTGGMDELYK"	rce 1711 /organism="synthetic const /mol_type="other DNA" /db_xref="taxon:32630" 1711 /note="mBanana; engineered	E 2 (bases 1 to 711) Shaner, N.C., Campbell, R.E., Steinbach, P.A., Palmer, A.E. and Tsien, R.Y. Direct Submission L Submitted (06-JUL-2004) Pharmacology, University of California, Submitted (06-JUL-2004) Submission CA 92093-0647, USA Diego, 9500 Gilman Dr., La Jolla, CA 92093-0647, USA	synthetic construct  SM synthetic construct  other sequences; artificial sequences.  1 (bases 1 to 711)  S Shaner, N.C., Campbell, R.E., Steinbach, P.A., Giepmans, B Palmer, A.E. and Tsien, R.Y.  Improved monomeric red, orange and yellow fluorescent derived from Discosoma sp. red fluorescent protein  Nat. Blotechnol. 22 (12), 1567-1572 (2004)  D 15558047	AY678267 711 bp DNA linear SYN 17-DEC-2 N Synthetic construct monomeric yellow-orange fluorescent protein gene, complete cds. AY678267 1 GT.55420620	ABRICIA BUTTALIST AND A STATE	LeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIleTyrMetAlaLys

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Ş	47 LygValThrLygGlyGlyFroLeuProPheAlaTrpAsplleLeuSerProGlnPheGln 66
Db	154 AAGGTGACCAAGGGTGGCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCTGC 213
δ	67 TyrGlySerLygValTyrValLygHigProAlaAspIleProAspTyrLygLygLygLeuSer 86
B	214 TACGGCTCCAAGGCCTACGTGAAGCACCCCACTGGTATCCCCGACTACTTCAAGCTGTCC 273
Ş	87 PheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGlyGlyValValThr 106
뫄	274 TTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACC 333
Ş	107 ValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysValLysPheIleGly 126
В	334 GTGGCTCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGC 393
ð	127 ValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGlyTrpGluAlaSer 146
皮	394 ACCAACTTCCCCTCCGACGCCCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCC 453
Ş	147 ThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLys 166
В	454 TCCGAGCGGATGTACCCCGAGGACGGCGCCCTGAAGGCCGAGATCAAGATGAGGCTGAAG 513
Ş	167 LeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIleTyrMetAlaLysLysPro 186
В	514 CTGAAGGACGGCCACTACAGCGCCGAGACCAAGACCACCTACAAGGCCAAGAAGCCC 573
Ş	187 ValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAspIleThrSerHisAsnGlu 206
Db	574 GTGCAGTTGCCCGGCGCCTACATAGCCGGCGAGAAGATCGACATCACCTCCCACAATGAG 633
Ş	207 AspTyrThrIleValGluGlnTyrGluArgThrGluGlyArgHis 221
망	634 GACTACACTATCGTGGAATTGTACGAGCGCGCCGAGGGCCGCCAC 678

Search completed: January 12, 2006, 13:57:52 Job time: 3773 secs

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Listing first 500 summaries
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-Q=/Cgn2 1/USPTO spool p/US100065922/runat_10012006 162503 19106/app_query.fasta_1.391
-Q=/Cgn2 1/USPTO spool p/US100065922/runat_10012006 162503 19106/app_query.fasta_1.391
-DB=N Genneseq -Open-frastap -SUPRT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=500 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=69 -ALIGN=500
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006922 @CGN 1 1 1096 @runat 10012006 162503 19106 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model
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Copyright (c) 1993 - 2006 Compugen Ltd.
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ABA95921 ABA95921 ABA95920 AAD46270 AAD28207 ADC24127 ADF70404 ADL46204

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                                                                                                                                                                                                                                                                                                                                                                    The invention provides a nucleic acid encoding functional red fluorescent CC protein (II) that differs from the sequence of an Anthozoan red fluorescent protein by at least one amino acid substitution, and with different fluorescent properties. The red fluorescent protein of the invention can be expressed by standard recombinant methodology. (II) are used a fluorescent markers and FRET partners. It is used for identifying protein-protein interactions. (II) is also suitable for multiplexed fluorescent analysis and FRET-based applications using existing Aequorea fluorescent proteins. (II) has improved brightness, reduced spectral cross talk, and is rapidly and efficiently expressed in mammalian cells. The key mutations in the encoding nucleic acids provide improved folding, brightness, and create (II) with sharper, more defined excitation and emission peaks when expressed in mammalian cells. The present sequence represents the coding sequence of a Discosoma sp. drFP583 protein, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 83; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins for Fluorescence Resonance Energy Transfer (FRET) comprise functional red fluorescent proteins, and the encoding nucleic acids, key mutations for improving the proteins function.
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Protein destabilisation, linker molety; reporter molety; disease model; linear multimerised domain; -NH-ubiquitin protein endoprotease; transgenic animal; transgenic plant; dieease resistance; anthologa fluorescent protein; natural fluorescent protein; ss.
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                                                          CThe patent discloses optical methods and compositions for determining CC transmembrane potential across biological membranes in living cells. The CC method of determining the electrical potential across a membrane in a CC method of determining the electrical potential across a membrane in a CC biological system comprises introduction of two reagents, a first reagent CC comprising a hydrophobic fluorescent ion capable of redistributing from a CC first face of the membrane to a second face of the membrane in response CC face or the second face of the membrane in response CC capable of undergoing energy transfer by either donating or accepting CC excited state energy to the fluorescent ion. The membrane is then exposed CC capable of undergoing energy transfer between the reagents is CC measured and related to the membrane potential. The method is useful for CC detecting changes in membrane potential in subcellular organism of test CC membranes in biological systems. The method is used for screening of test CC memicals for activity to modulate the activity of target ion channel. CC reagent that comprises a charged hydrophobic fluorescent molecule and a second reagent comprising a bioluminescent or naturally fluorescent control of the present sequence is Discosoma species (red) DNA encoding an CA protein. The present sequence is Discosoma species (red) DNA encoding an comprising a first control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane potential; biological membrane; test chemical screening; Anthozoa fluorescent transgenic organism; drFP583 protein; ds.
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DB:
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Best Local Similarity:
Yeast; red fluorescent protein; RFP; plant; transgenic; GFP; Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana; Escherichia coli; green fluorescent protein; biotechnology; gene;
                                                Yeast
                                                                        29-MAY-2002
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to DNA (I) containing either sequence ABA95905 or sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (YRFP). (I) are used to express red fluorescent protein (RFP) in elekaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum or Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Escherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern biotechnology. (I) are optimised for expression in yeast and so generate RFP at higher levels with stronger fluorescence and thus lowers the detection limit and gives a better signal-to-noise ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding red fluorescent protein, useful as marker in biotechnology, has sequence optimized for expression in eukar especially yeast or plants.
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AspG1yG1yVa1Va1ThrVa1ThrG1nAspSerSerLeuG1nAspG1yCysPheI1eTyr 120
                                                                                      AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                                                              TTGTCTCCACAATTCCAATACGGTTCTAAGGTCTACGTCAAGCACCCAGCTGACATTCCA
                                                                                                                                                                        LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                                                                                  CACAACACTGTCAAGTTGAAGGTTACTAAGGGTGGTCCATTGCCATTCGCTTGGGACATC
                                                                                                                                                                                                                                                        HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
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The invention relates to DNA (I) containing either sequence ABA95905 of sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (yRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Escherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern
                                                                                                                                      New DNA encoding red fluorescent protein, useful as marker in biotechnology, has sequence optimized for expression in eukaryotes, especially yeast or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast; red fluorescent protein; RFP; plant; transgenic; GFP; Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana Escherichia coli; green fluorescent protein; biotechnology; gene;
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The invention relates to DNA (I) containing either sequence ABA95905 sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (yRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum
                                                                                                                                                                                                                                                      New DNA encoding red fluorescent protein, biotechnology, has sequence optimized for especially yeast or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast; red fluorescent protein; RFP; plant; transgenic; GFP; Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana; Escherichia coli; green fluorescent protein; biotechnology; ss.
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                                                                                     US-10-006-922A-12 (1-225) x AAD46278 (1-678)
                                                                                                                              Query
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Best Local Similarity:
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                                                                                                                                                                                                                                                              The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is DNA encoding Discosoma sp. drFP583 (NFP-6) wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Chidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 70; 80pp; English.
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P-PSDB; AAE28833.
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04-DEC-2001;
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                                                                                                                                                                                                                            Sequence 678 BP; 146 A;
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                                                                                                                                 Match:
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ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                    MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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                                                                                                                                                                                                                                                        the invention
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2001US-00006922.
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          Fradkov
                                                                          13-JUN-2001; 2001WO-US019097.
                                                                                                                      WO200196373-A2
                                                                                                                                                                                                   Discosoma
                                                                                                                                                                                                                       Fluorescent timer protein; protein movement; translocation; trafficking; promoter activity; gene expression; transgenic plant; gene modification; protein age; anthozoa protein; drFPS83; ds.
                               (CLON-) CLONTECH LAB INC.
                                                                                                 20-DEC-2001.
                                                                                                                                                                                                                                                                    Discosoma sp. humanised wild-type Anthozoa protein drFP583 DNA
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          ΑF,
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                                                                                                                                                                                                                                                                                                                                     standard; DNA; 678
                                                                                                                                                                                                                                                                                                                                                                                  CACCACCTGTTCCTG
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          Terskikh A;
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WPI; 2002-154595/20.
P-PSDB; AAE17540.
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New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking

Example 1; Fig 1; 89pp; English.

The invention relates to a fluorescent timer protein having an emission expectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer proteins are useful in comitoring the activity of a promoter, determining the age of a protein, comitoring the activity of a promoter, determining the age of a protein, comitoring an agent that modulates the activity of a promoter and in conversion during development of cells comprising a fluorescent timer protein. Compression during development of a multicellular organism or during compression during comprising a fluorescent timer protein. Compression during development of a multicellular organism or during compression during compression to a drug or other inducer of compression trafficking, or protein sate also useful for assessing gene cativity, monitoring intracellular protein movement or translocation, compress of the activity of a regulatory element, for determining cell caspects of the activity of a regulatory element, for determining cell compression trafficking, or protein stability, to investigate temporal compression of newly synthesised proteins and accumulated proteins, and combrane junctions and extracellular matrix components. The fluorescent combrane junctions and extracellular matrix components. The fluorescent components in prokaryotic and eukaryotic cells, in protease cleavage as biosensors in prokaryotic, non-human plants or animals or site specific gene codifications in cell lines. The present sequence is a DNA encoding components of humanised wild-type Anthozoa protein dripps used for generating fluorescent proteins

Sequence 678 BP; 146 A; 223 C; 203 G; 106 7 0 U; 0 Other;

δ 밁 S 밁 ठ 밁 ঠ 밁 S ₽ S Percent Similarity:
Best Local Similarity:
Query Match: 밁 US-10-006-922A-12 (1-225) x AAD28207 (1-678) Alignment Scores: Pred. No.: 101 241 181 121 81 61 41 61 21 AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120 GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG 300 LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAapIlePro 80 CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCTGCCCTTCGCCTTGGGACATC HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60 ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCCGAGGGCCGAGGGCCCCCTACGAGGGC 120 ATGCGCTCCTCCAAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100 CTGTCCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGGCCGACATCCCC ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40 2.3e-140 1214.00 100.00% 100.00% 100.00% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

60

240

180

121 LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140

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RESULT 10
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XX ADC24
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XX Filoo
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XX Disco
XX Filoo
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DR CAMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Discosoma red fluorescent protein; DsRed; AB interface; AC interface; fluorescent protein variant; transcription induction detection; fluorescence energy resonance transfer; FRET; protein kinase; protein phosphatase; ion indicator; ds.
The invention describes a polynucleotide sequence (I) encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerise, comprising amino acid substitutions at the AB and/or AC interfaces of the wild-type DsRed sequence (SI) comprising 225 amino acids, given in the specification, where the substitutions result in reduced propensity of the DsRed variant to form tetramers. (I) is useful for detecting transcriptional activity by providing a host cells constlning a vector which comprises (I) operatively linked to an expression control sequence, and an unit to assay the variant fluorescent protein fluorescence, and assaying fluorescence of the variant
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24-MAY-2001; 2001US-00866538.
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                                                                                                                                                                                                                                                                                                                                                                transcriptional activity.
                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-743764/70.
P-PSDB; ADC24126.
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                                                                                                                                                                                                                                                                                                          Example 1;
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(CAMP/) CAMPBELL R
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9999999999999999999988 CC fluorescent protein produced by (VII), where variant fluorescent protein CC fluorescence is indicative of transcriptional activity. A polynucleotide CC encoding a fusion protein is useful for the analysis of in vivo CC localisation or trafficking of a polypeptide of interest. A polypeptide CC marker is useful as markers to identify the location and amount of a CC target protein produced, where the target protein is fused to the marker, CC as a complement to or alternative for the green fluorescent protein or CC its spectral variant, for detecting induction of transcriptions, in CC which detects events as the function of the movement of fluorescent General detects events as the function of the movement of fluorescent CC fluorescent sensors for protein kinase and phosphatase activities or CC indicators for lons and molecules such as Ca2+, Zn2+, for identifying the presence of a molecule in a sample, for identifying a specific interaction of a first and second molecule, for determining whether a CC useful for identifying a region or condition that regulates the activity of an expression control sequence. This sequence encodes Discosoma wild-type red fluorescent protein.

678 B₽; 205 A; 129 ü 178 ٠ G 166 T; 0 U; 0 Other

Alignment

Дb	Qy	뮹	\$	US-10-006-922A-12 (1-225) x ADC24127 (1-678)	DB:	Query Match:	Best Local	Percent Similarity:	Score:	Pred. No.:	The state of the s
61 ACGGTCAAT	21 ThrValAsn	1 ATGAGGTCT	1 MetArgSe         1 ATGAGGTC			::	Best Local Similarity:	ilarity:			
GGCACGAGTTTG	5) x ADC24127 SerLysAsnValI           TCCAAGAATGTTF TCCAAGAATGTTF	cSerLysAsnVal              TCCAAGAATGTT	SerLysAsnVal:	10	100.00%	100.00%	100.00%	1214.00	2.3e-140		
21 ThrValAsmGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40	MetArgSerSerLysAgnVall1eLysGluPheMetArgPheLysValArgMetGluGly 20	(1-678)	Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:			
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120	40	. 60	20								

8 밁 S S 문 á 밁 5 片 S 밁 ঠ 밁 Ś 밁 밁 161 421 141 361 121 301 101 241 181 121 81 61 41 HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr GACGGTGGCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTAC AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr GACTATAAAAAGCTGTCATTTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACTTTGAA TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGACCTTTGCCATTTGCTTGGGATATT IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp AAGGTCAAGTTCATTGGCGTGAACTTTCCTTCCGATGGACCTGTTATGCAAAAGAAGACA ATTCATAAGGCTCTGAAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAAGTATT <u>ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTTGAAAGGAGAG</u> 200 180 160 140 120 100 240 80 180 60 600 540 480 420 360 300

60 120

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RESULT 11
ADP70404
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                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPuv or Enhanced GFP (BGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligand; orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP, GFPuv; Enhanced GFP; EGFP; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 27; 594pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transformation of cells with a fusion protein of an orphan receptor protein with a fluorescent protein useful for identification of ligands
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23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
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29-JUL-2002;
                                                                                                                                    09-APR-2003;
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2002US-00121258.
2002US-00209208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fluorescent protein; DsRed; fluorescence; red wavelength; on; tetramerization; immunoassay; hybridization assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DBRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DBRed sequence, where the substitutions result in reduced propensity of the DBRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DBRed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 678 BP;
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AspG1yG1yVa1Va1ThrVa1ThrG1nAspSerSerLeuG1nAspG1yCysPheIleTyr
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                                              ATGGGCTGGGAAGCCACCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTTGAAAGGAGAG
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CC fluorescent protein or its mutant. The protein is useful in applications consequence in protein or its mutant. The protein is useful in applications consequence in the protein is useful in applications consequence in the protein is expressed, and isolating the cell, whereby the protein is expressed, and isolating the compositions involving chrome or fluorescent protein and is useful in complications involving chrome or fluorescent protein and is useful in complications involving chrome or fluorescent protein and is useful in compositions, hybridization probes, etc. The expression cassettes are composition of matter e.g. food compositions, are useful compositions, planta conditions, conditions, planta conditions, conditions, planta conditions, conditions, planta conditions, conditions, proteins find use in a variety of different applications, as biosensors in prokaryotic and eukaryotic cells, in applications involving the automated screening of arrays of cells expressing fluorescent conditions, as second messenger detectors, and in fluorescence activated cell sorting applications and as in vivo marker in animals. The fluorescent proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid encoding a rapidly maturing chromo- or fluorescent mutant of a Chidarian chromo- or fluorescent protein or its mutant, useful for applications involving chromo- or fluorescent proteins.
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                                                                                                                                 IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                                                                     TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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                                                                                                                                                                                                                                                                                                          GACGGTGGCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTAC
                                                                                                                                                                                                                                                                                                                   AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                                                                                                                                                                                                                              GACTATAAAAAGCTGTCATTTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACTTTGAA
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                                                                                                                       ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAAGAACCGAGGGACGC
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel binding ligand with intrinsic fluorescence and comprising fluorescent protein having heterologous binding sites, useful for detecting target molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 678 BP;
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                    AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                      LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                                                               ACGGTCAATGGGCACGAGTTTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGC
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                                                                                                                                                                                                                                                                                                                            ds; gene; enzyme; sensor cell; fluorescent protein;
signal transduction detection system; promoter; targeting sequence;
targeted drug.
                                                          Developing a sensor cell, useful in determining the activity of a target gene and in developing therapeutic drugs, comprises providing cells comprising a signal transduction detection system and introducing DNA
                                                                                                                                                                         05-SEP-2002; 2002US-0408297P
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                                                                                                                                                                                                                                                                                                          Discosoma sp.
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                              Disclosure;
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 present invention relates to a method of developing a sensor determining the activity of a target gene in the cell, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;
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                   HisHisLeuPheLeu
                                                                       ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAAGAACCGAGGGACGC
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                                                                                                                                              TACATGGCAAAGAAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAAACTGGAT
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                                                                                                                                                                                                                                                                                                                                                         The present sequence is humanised drFP583 cDNA drFP583 is a full-length CC cDNA encoding a novel fluorescent protein (nFP) from Discosoma sp. "red", CC a non-bioluminescent species of the Class Anthozoa. The wild-type drFP583 CCC nucleotide sequence was altered to optimise the codons for expression of CC the fluorescent protein in mammalian cells. Fluorescent proteins can be used in fluorescent labeling, a useful tool for marking a protein, cell cor organism of interest. Unlike other markers used in protein labeling, cell crequire an exogenous cofactor or substrate. Methods involving fluorescent crequire an exogenous cofactor or substrate. Methods involving fluorescent correctins are also less laborious and less difficult to control than the craditional methods of fluorescent labeling, where a protein of interest is purified and then covalently conjugated to a fluorephore derivative. CC is purified and then covalently conjugated to a fluorephore derivative can be used as markers for gene expression and protein localization constitutes, and in fluorescence resonance energy transfer (FRET) reactions. They may have improved properties and better suitability for larger constitutions compared to prior art fluorescent proteins such as green
                                                                                                                                                                                                                                                                                                                  Sequence 695 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 75-76; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel fluorescent protein from non-bioluminescent Discosoma
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14-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                 fluorescent protein
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HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
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WPI; 2002-539633/58.
P-PSDB; AAO18270.
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                                                                             Lichtenberg-Frate H;
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Modified yeast strain, useful for detecting toxic compounds in environment, contains integrated cassettes responsive to genotoxic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 20-21; 34pp; German.
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                                                   TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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                                                  This invention relates to a novel non-oligomerizing fluorescent protein. CC Specifically, it refers to the presence of at least one mutation in the CC fluorescent protein that reduces or eliminates the ability of the protein CC to oligomerize. The present invention describes fluorescent proteins CC derived from naturally occurring green or red fluorescent proteins and CC provides a fusion protein that comprises a non-oligomerizing fluorescent CC protein linked to at least one protein of interest. As such, these fusion CC proteins can be used in methods and compositions to determine the pH of a CC sample, or whether the sample contains an enzyme, molecule or agent that CC they may be used to identify a specific interaction of molecules, such CC that they are useful for improving or developing new assays in the field CC of molecular biology. This polynucleotide is the DNA sequence that invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non-oligomerizing fluorescent protein containing at least one mutation that reduces or eliminates the ability of the protein to oligomerize, useful for making better and new assays for molecular
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                                                                                                     Discosoma
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                                                                                                                                                                             Discosoma
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                                                                                                                                                                          species red fluorescent protein (RFP) encoding
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                                                         Location/Qualifiers 54. .731
                               /product= "Discosoma sp. red fluorescent protein (RFP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Discosoma species red fluorescent protein (RFP) encoding DNA used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
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                                                AAGGTCAAGTTCATTGGCGTGAACTTTCCTTCCGATGGACCTGTTATGCAAAAGAAGAACA
                                                               LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                        GACGGTGGCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTAC
                                                                                                                       AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
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Alignment Scores:
                                                                                     The invention relates to a non-oligomerising fluorescent protein containing a mutation that reduces or eliminates its ability to oligomerise. The fluorescent protein gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction, enzymes, or sample pH. These are also used to identify agents or conditions that regulate expression of control sequences. The present sequence is Discosoma sp. red fluorescent protein (RFP) cDNA
                                                                                                                                                                                                                                                                                                                                                          Pluorescent proteins containing a mutation that reduces or eliminates is ability to oligomerize which gives more reliable fluorescence resonance energy transfer results and are useful to detect molecule interaction,
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P-PSDB; ABW00918.
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                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a chimeric phosphorylation indicator (CPI) (I) comprising in operative linkage, a first fluorescent protein, a phosphoaminoacid binding domain with an FHAZ sequence defined in the specification, a protein kinase C (PKC)-phosphorylatable domain, and a second fluorescent protein. The first and second fluorescent proteins are chosen from green fluorescent proteins (GFPs) and red fluorescent proteins are detectable resonance energy transfer, when the first fluorescent protein is excited. The FKC-phosphorylatable domain and phosphoaminoacid binding domain do not substantially emit light to excite the second fluorescent protein is sexited. (I) is useful for detecting a protein kinase C (PKC) or phosphates in a sample (such as biological sample e.g. cell, tissue sample, or their extracts). (I) is useful for detecting a kinase inhibitor or phosphatase inhibitor. The method of the invention is adapted to high throughput analysis. The current sequence represents the
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31-JAN-1997;
13-SEP-1999;
24-MAY-2001;
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                     Simultaneously quantifying in situ the relationship between an enzyme its substrate for study of enzymatic processes at a cellular level, comprises optical measurements on cells expressing the fluorescently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fluorescently-tagged enzyme; substrate; cell population; GFP; quantification of enzymatic activity; green fluorescent protein; red fluorescent protein; RFP; enhanced green fluorescent protein; enzymatic process; cellular enzyme; chemotherapeutic drug;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for simultaneously quantifying in situ the relationship between a fluorescently-tagged enzyme (E) and it substrate in a population of cells. A population of cells expressing (E) is created in which different cells contain different amounts of (E). The cells are incubated with a substrate, and the concentration and cenzymatic activity of (E) in each cell are simultaneously quantified by optical means. The fluorescently-tagged enzyme is produced by linking the cenzyme with Aequorea victoria green fluorescent protein (GFP), or its carried green fluorescent protein (GFP), or its carried green fluorescent protein (GFP), and cenzyme and its substrate in a cell. The method of the invention is carryme and its substrate in a cell. The method is useful for the study of enzyme and its substrate in a cell. The method is useful for the study of the interactions of cellular level, and especially for examining the interactions of cellular enzymes with chemotherapeutic drugs, e.g. for elucidating mechanisms of multidrug resistance (MDR). The present ground containing the coding sequence for RFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3311 BP; 858 A; 778 C;
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The invention describes a polynucleotide sequence (I) encoding a CC Discosoma red fluorescent protein (DsRed) variant having a reduced CC propensity to oligomerise, comprising amino acid substitutions at the AB CC and/or AC interfaces of the wild-type DsRed sequence (SI) comprising 225 cm and no acids, given in the specification, where the substitutions result CC in reduced propensity of the DsRed variant to form tetramers. (I) is CC useful for detecting transcriptional activity by providing a host cells conatining a vector which comprises (I) operatively linked to an CC expression control sequence, and an unit to assay the variant fluorescent grotein fluorescence, and assaying fluorescence of the variant fluorescent fluorescent protein produced by (VII), where variant fluorescent protein fluorescence is indicative of transcriptional activity. A polynucleotide concading a fusion protein is useful for the analysis of in vivo CC marker is useful as markers to identify the location and amount of a cc as a complement to or alternative for the green fluorescent protein or trafficking of a polypeptide of interest. A polypeptide cas a complement to or alternative for the green fluorescent protein or the spectral variant, for detecting induction of transcriptions, in CC which detects events as the function of the movement of fluorescent condicators for ions and molecules such as Ca2+, Zn2+, for identifying the presence of a molecule in a sample, for identifying a specific condicators for ions and molecules such as Ca2+, Zn2+, for identifying the gressence on fairst and second molecule, for determining whether a condicators for ions and molecules such as Ca2+, Zn2+, for identifying the gressence on fairst and second molecule, for determining whether a condicators for ions and molecules such as Ca2+, Zn2+, for identifying the gressence on fairst and second molecule, for determining whether a condicators for molecule and for determining whether a condicators for molecule and for determining the pluorescent condicators for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; ADC24126.
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24-MAY-2001; 2001US-00866538.
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CAMPBELL R
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ds; gene; red fluorescent protein; DsRed; fluorescence; red wavelength; oligomerization; tetramerization; immunoassay; hybridization assay. Human codon optimised Discosoma red fluorescent protein (DsRed)

WO2003086446-A1

23-OCT-2003

09-APR-2003; 2003WO-US010879

10-APR-2002; 2002US-00121258. 29-JUL-2002; 2002US-00209208.

(REGC ) UNIV CALIFORNIA

Tsien RY, Campbell RE, Baird gs

WPI; 2003-845265/78.

New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, usefin molecular biology, e.g. in immunoassays or in tracking protein movement in cells. useful

Disclosure; SEQ ID NO 3; 166pp; English

The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed coding sequence with codons optimised for human expression.

Sequence 681 BP; 146 A; 223 C; 205 G; 107 7 0 U; 0 Other;

Query Match: Percent Similarity: Best Local Similari Pred. Alignment Scores: М : Similarity: 7.26e-140 1210.00 100.00% 99.56% 99.67% Mismatches: Indels: Matches: Conservative: 0 0 0 0

US-10-006-922A-12 (1-225) x ADL46205 (1-681)

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     The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DeRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DeRed sequence, where the substitutions result in reduced propensity of the DeRed variant to form tetramers and where the variant displays detectable
                                                                                                                                                                                                                                            New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful in molecular biology, e.g. in immunoassays or in tracking protein movement in cells.
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                                                                                                                                                                                              Disclosure, SEQ ID NO 23; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 681 BP; 146 A; 223
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ABZ22476 standard; DNA;

ABZ22476;

Mammalian 25-MAR-2003

codon

optimised Discosoma red fluorescent protein

DNA.

(first

entry

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Alignment
Pred. No.:
Score:
   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                  The present invention describes an isolated Discosoma red fluorescent CC protein (1) comprising a 241 residue amino acid sequence (see ABP56678, CC S1), with one or more point mutations at amino acid position N24, F125, CC K164, or M183. Also described: (1) a fusion protein comprising (1); (2) CC an isolated nucleic acid encoding (1); (3) a vector comprising the CC nucleic acid of (2); (4) a host cell comprising the vector; (5) a CC retroviral cDNA expression library comprising the nucleic acid of (2), or CC encoding (1); and (6) methods of making a fluorescent variant. The CC piscosoma red fluorescent proteins are useful for functional screens as a CC reporter for gene transcription (e.g. as a fusion protein), for target CC characterisation and localisation of fusion proteins, or for scaffolds CC characterisation and localisation of fusion proteins, or for scaffolds CC used as selectable markers or reporter molecules for a variety of CC used as selectable markers or reporter molecules for a variety of CC used as selection mechanism. The method of directed protein evolution CC useful for obtaining improved variants of red fluorescent protein. The CC variants of Discosoma red fluorescent protein have greatly improved CC variants, expression, and/or folding kinetics as compared to wild type or a codon optimised variant. The present sequence encodes a mammalian CC compared to protein reporter reporter in which is used in an angular form the present sequence encodes a mammalian compared to manufacian red fluorescent protein, which is used in an angular form the present sequence encodes a mammalian compared to wild type or a codon optimised variant. The present protein, which is used in an account of the present sequence encodes a mammalian compared to wild type or a codon optimised variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Discosoma red fluorescent protein, useful for functional screens as reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptic
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/transl_except= (pos:616. .618,aa:His)
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Best Local S:
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The present invention describes a chimeric protein comprising at least one signal protein that has a trafficking signal targeting to a subcellular organelle and at least one proteolytic leavage site for a protease. The chimeric protein is constructed, so that: (a) the trafficking signals of all the signal proteins are inactivated by linking the proteolytic site or a signal masking protein through the proteolytic
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Human immunodeficiency virus
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Best Local Similarity:
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                    New nucleic acid that directs expression of protein in silk glands of silkworm, useful for preparation of pharmaceutical proteins and for modifying textile properties of silk.
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                                                                                                                                                 Couble I
                                                                                                                                                                                                                  CENT NAT RECH SCI.
LYON 1 BERNARD CLAUDE.
INST NAT RECH AGRONOMIQUE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
/note= "Binding site
-~~ forkhead type"
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/note= "Fibrohexamerin intron
2041. .2721
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/note= "This region
1362. .1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Reporter protein Ds-Red
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, Royer
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                                                                                                                                                        C, A
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                                                                                                                                                                            Julien
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50pp; French

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Percent Similarity:
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                                                                                                                  GACGGCGGCGTGATCACCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
                                                                                                                                                                                                                                                                           AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                                                                                                                                                                                                         GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
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AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACC
                                                    ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
                                                                          IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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99.67%
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                   New nucleic acid that directs expression of protein in silk silkworm, useful for preparation of pharmaceutical proteins modifying textile properties of silk.
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                                                                                                                                                                             WPI; 2004-670997/66.
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                                                                                                                                                                                                                                                                                       CENT NAT RECH SCI.
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INST NAT RECH AGRONOMIQUE.
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                                                                                                                                                                                                                    Couble P, Durand B, Nony P, Prudhomme JC,
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1577. .2077
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ranscription factors of the SGF1 forkhead type"
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1092. .2772
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'note= "Fibrohexamerin
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abel= Fibrohexamerin
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The present invention relates to a novel nucleic acid (I) that directs

Example 3; SEQ ID NO 3; 50pp; French

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-006-922A-12 (1-225) x ADS75468 (1-2772)
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TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrTalAapSerLysLeuAsp 200
                                                                                                                 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
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                                                                                         US-10-006-922A-12 (1-225) x AAL47954 (1-4692)
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                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a modified yeast strain that contains, integrated stably and functionally in its genome, a genotoxicity cassetter and a cytotoxicity cassette, each comprising a promoter and reporter gene, both of which are different in the two cassettes. The modified yeast strain is used to detect environmental pollution, especially genotoxic and/or cytotoxic substances in complex environmental contaminants, especially organic compounds, but also (non-)ionising radiation and chemical carcinogens. Particular applications are in monitoring (waste) water (e.g. as an early warning system), medical toxicology screening and for industrial process control. The present sequence is a vector suitable for use in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified yeast strain, useful for detecting toxic compounds in environment, contains integrated cassettes responsive to genotoxic cytotoxic compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4692 BP; 1111 A; 1268 C; 1247 G; 1066 T; 0 U;
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 Perkins
Stewart
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                                                                30-MAY-2001; 2001US-0294758P
21-MAR-2002; 2002US-0366891P
                                                                                                                                                                                       Discosoma sp. Synthetic.
                                                                                                                                                                                                                                                                                  Vector pDsRed1N1 nucleotide sequence SEQ ID NO:29
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                                          (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
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Query Match:

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Length:
Matches:
Conservative:
Mismatches:

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Gaps: Indels: Score: Alignment

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cone or several att sites, where an att site is heterologous to the CC chromosome, and permits site-directed integration in the presence of CC lambda-integrase. Also described: (1) a platform artificial chromosome CC introducing a heterologous mucleic acid into a platform artificial chromosome CC introducing a heterologous mucleic acid into a platform artificial CC chromosome. (1) can be used in gene therapy. (M1) is useful for CC introducing a heterologous mucleic acid molecule into a platform cC artificial chromosome, preferably an Aces. (II) is useful for CC artificial chromosome, preferably an Aces. (II) is useful for producing a troducing (II) by cell fusion, lipid-mediated transfection CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, comicroprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous concleic acid that encodes a therapeutic product which is useful for caking a library of Aces comprising random portions of a genome. ACC44612 can ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention
Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 182-184; 272pp; English
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Sequence 4692 BP; 1111 A; 1268 C; 1247 G; 1066 H, 0 ď 0

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The invention relates to a construct which allows animals to be bred in captivity but renders them infertile in the wild by allowing reversible control over fertility and reproduction. The construct comprises a native promoter, a blocking DNA sequence contoured for and designed to abrogate a crucial gene's function or to cause its mis-expression, and a genetic switch to regulate controlled expression/repression of the blocker/gene knockout. The construct is useful for preventing embryogenesis or gametogenesis in animals by stably transforming an animal cell with the construct by microinjection, transfection or infection, where the construct stably integrates into the genome by homologous recombination, and implanting the cell into a host organism, where a whole animal develops from the implanted cell. The present sequence is plasmid pSFM 6 containing mouse goosecoid promoter expressing goosecoid cDNA fused to red fluorescent protein. The plasmid contains CMV promoter and SV40 polyA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel construct for preventing embryogenesis in animals comprises promoter, blocking DNA which abrogates function of crucial gene ar genetic switch to regulate expression/repression of blocker/gene
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detecting site-specific DNA recombination in eukaryotic cells. Recombination with Cre recombinase lacking heterologous protein-transduction domains is used for therapeutic site-specific recombination
                       This invention describes a novel method of site-specific DNA recombination in eukaryotic cells in vitro comprising using a bacteriophage P1 Cre recombinase that lacks heterologous protein-transduction domains. The invention also contains a reporter system
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chromosomal translocation; reporter protein; ds; circular.
                                                                                       In vitro or in vivo site-specific DNA recombination, useful e.g. for gene inactivation, using Cre recombinase that lacks heterologous protein-
                                                                                                                                                (VISI-) VISION 7 GMBH
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note= "MPSV 5'-LTR (Delta-31)"
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                                                                                          US-10-006-922A-12
                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel construct for preventing embryogenesis in animals comprises native promoter, blocking DNA which abrogates function of crucial gene and genetic switch to regulate expression/repression of blocker/gene
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                                                                                                             /product= "puromycin
2267. .2848
                                       /note= "CMV promoter 2906. .3348
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product= "N'-EGFP"
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                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel vector containing, at least, two CC composes DNA sequences that, through DNA exchange, induce a change in a CC gene present in the vector. The products of the invention are used to CC assess genotoxicity of compounds (e.g. components of foods, cosmetics and medicines), to determine susceptibility for development or progression of CC cancer, for analysis of (non-)conservative recombination processes, end CC joining and inactivating/reverting mutations, for characterization of CC selected genes with respect to maintenance or reduction of genetic compatibility, and to determine genetic (in) stability and recombinational or CC mutational frequency of cells, tissues or organisms. The vector allows an CC contine use), and can be used with a variety of eukaryotic cells and CC contine use), and can be used with a variety of eukaryotic cells and CC contine use), and can be used with a variety of eukaryotic cells and CC contine use), and can be used with a variety of eukaryotic cells and CC contine use), and can be used with a variety of eukaryotic cells and CC contine use), and can be used with a variety of eukaryotic cells and CC contine use) and can be used with a variety of eukaryotic cells and CC content and can be used with a variety of eukaryotic cells and CC content and can be used with a variety of eukaryotic cells and CC content and can be used with a variety of eukaryotic cells and CC content and can be used with a variety of eukaryotic cells and CC described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vector containing recombination sequences, useful e.g. for assessing compounds for genotoxicity, cancer susceptibility and mutational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; vector; transposase; promoter; insertion sequence; Kozak; Tn10; ovalbumin; vitellogenin; polyA; conalbumin; enhancer; ovomucoid; signal sequence; transgenic animal; Huntington's disease; alpha-1-antitrypsin deficiency; Alzheimer's disease; breast cancer; cystic fibrosis; galactosaemia; congenital hypothyroidism; cystic fibrosis; galactosaemia; congenital hypothyroidism;
                                                                                                                                                                                                                                                                                                                                                                                                                           maple syrup urine disease; neurofibromatosis; phenylketonuria; sickle cell disease; Smith-Lemli-Optiz Syndrome; autoimmune disease; shipping fever; cattle; mastitis; bacterial; viral; infection; Types I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector pTnMod (Oval/Red) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI04104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI04104 standard;
  misc_feature
                                                                                promoter
                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                     shipping fever; cat
type; II; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGGCGGCGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrmetālaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp 200
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                                                                                                                                                                         /"cag= a
/note= "Remainder of F
131. .132
  /note= "CMV promoter/enhancer from pGWiz" 1778. .1779
                                                                                used in construction"
133. .1777
                                                                                                                               /*tag= b
/note= "Residue from ligation
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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                                                                                                                                          윩
                                                                                                                                                                                                                     from pBluescript11 sk(-)"
                                                                                                                                          restriction enzyme sites
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                                                                                                                                                                                                                                                                                                                                                           promoter
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insertion_seq
                                   misc_signal
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/note= "Residue from ligation of restriction enzyme sites
used in construction"
1780. .2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Two
2995. .3410
         /note= "Residue from ligation of restriction enzyme sites
used in construction"
                                                                         /note= "Residue from ligation of used in construction"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Residue from ligation of restriction enzyme sites
used in construction"
                                                                                                                                                                                                                           /*tag= q
/note= "Residue from
used in construction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3719. .3761
                                                                                                             note= "Multiple
                                                                                                                                                  /*tag= s
/note= "Residue from ligation
/note in construction"
                                                                                                                                                                                                                                                                                                                               note= "Japanese quail ovalbumin promoter"
note= "Includes steroid-dependant respons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Left insertion sequence recognised by Tn10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Non-coding DNA residual from pNK2859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Taken from pGWiz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product= "Transposase"
note= "Modified from T
                                               note= "Multiple cloning site
                                                                                                                                                                                                 note= "DsRed
                                                                                                                                                                                                                                                                note= "Japanese quail ovalbumin
                                                                                                                                                                                                                                                                                                    note= "Residue from ligation of
                                                                                                                                                                                                                                                                                                                                                                                                         note= "Multiple cloning site from pBluescipt11 sk(-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Non-coding lambda DNA residual from pNK2859"
                                                                                                                                                                                     Le= "DBRed reporter coding sequence including polyAn DDREd1.1"
                                                                                                                                                                                                                                                                                                                                                                              e= "Residue from ligation of restriction enzyme sites
                                                                                                                                                                                                                                                                                   in construction"
                                                                                                                                                                                                                                                                                                                                                                    in construction"
                                                                                                    .6042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3837
                                                                                                                                           .6036
                                                                                                                                                                                                                                                        .5098
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                                                                 . 6475
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                                                                                                                        cloning
                                                                                                                                                                                                                                     ligation of restriction enzyme sites
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                                                from
                                                                                    restriction enzyme sites
                                                                                                                                                                                                                                                                signal sequence"
                                                                                                                                                             restriction
                                                                                                                                                                                                                                                                                                      restriction enzyme sites
                                               pBluescript11 sk(-)"
                                                                                                                                                                                                                                                                                                                                response element"
                                                                                                                         ZeroBlunt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codons
                                                                                                                                                             enzyme sites
                                                                                                                        Topo cloning
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CC promoter, which is a constitutive promoter or an inducible promoter, e.g. can ovalbumin or a vitellogenin promoter. The vector further comprises a copoly a sequence, a conalbumin poly a sequence, operably linked to the transposase gene. The vector further comprises two stop codons operably comprises the second gene of interest is coperably linked to a second or third promoter, respectively. The first and a second gene of interest are operably linked to a second promoter. The vector further comprises an enhancer operably linked to the one or compressed in terest. The enhancer comprises at least a portion of an covalbumin enhancer. The vector further comprises an egg directing covalbumin enhancer. The vector further comprises an egg directing covalbumin enhancer, operably linked to the one or covalbumin enhancer. The vector further comprises an egg directing converting sequence, ovalbumin or ovomucoid signal sequence or vitellogenin contains such desired contains or molecules. They are also useful in treating Huntington's concerning the contains with desired the contains of the vector is called a concentral hypothyroidism. maple concerning the contains of the vector is called a concentral throughtyroidism. maple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2003;
21-JAN-2003;
21-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                       gene operably linked to a first promoter and one or more gene of interest operably linked to one or more additional promoters, where the one or more genes of interest and their operably linked promoters are flanked by transposase insertion sequences recognized by the transposase and the first promoter comprises a modified Kozak sequence comprising ACCATG. The transposase is a Tn10 transposase and is modified in one to twenty of the first codons. The gene of interest in operably linked to a second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New vector comprising a transposase gene operably linked to a promoter, useful in treating Alzheimer's disease, breast cancer, phenylketonuria, autoimmune diseases, bacterial or viral infections or Types I and II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                     cancer, cystic fibrosis, galactosaemia, congenital hypothyroidism, maple syrup urine disease, neurofibromatosis, phenylketonuria, sickle cell disease, Smith-Lemli-Optiz Syndrome, autoimmune diseases, shipping fever in cattle, mastitis, bacterial or viral infections or Types I and II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a new vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 4; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-083042/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cooper RK,
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21-JAN-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes.
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UNIV LOUISIANA STATE & AGRIC & MECH COLL
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2003US-0441447P
2003US-0441502P
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2003US-0441392P
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6551.
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6593.
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= "Right
.6592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fioretti WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insertion sequence recognised by Tn10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deboer KF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pTnMod, comprising a transposase
er and one or more gene of interest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residual from pNK2859
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Alignment Scores: Pred. No.:

3.04e-138

Length:

9658

Sequence 9658

BP;

2572 A;

2397

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2148 G;

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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
RESULT 38
ADI04103
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ss; vector; transposase; promoter; insertion sequence; Kozak; Tn10; ovalbumin; vitellogenin; polyA; conalbumin; enhancer; ovomucoid; signal sequence; transgenic animal; Huntington's disease; sleast cancer; alpha-1-antitrypsin deficiency; Alzheimer's disease; breast cancer; cystic fibrosis; galactosaemia; congenital hypothyroidism; maple syrup urine disease; neurofibromatosis; phenylketonuria; sickle cell disease; Smith-Lemli-Optiz Syndrome; autoimmune disease
                                                                                                                      Vector pTnMod
                                                                                                                                                   22-APR-2004
                                                                                                                                                                               ADI04103
                                                                                                                                                                                                             ADI04103 standard;
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                                                                                                                                                                                                                                                                                                      HisHisLeuPheLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
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99.67%
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Mismatches:
Indels:
Gaps:
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1. .130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in construction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Residue from ligation used in construction"
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/note= "Residue from ligation
used in construction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Residue from ligation used in construction"
                                                                                                                                                                                                    used in construction" 4050. .4951
                                                                                                                                                                                                                                                                           /note= "Multiple cloning site
/note= "May be used to insert
into the vector"
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    /*tag= r
/note= "DsRed reporter
from pDsRed1.1"
                                                                                /*tag= q
/note= "Residue
                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Left
                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Non-coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Residue from ligation
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/note= "Modified from T)
                                                                                                                          note= "Chicken
                                                                                                                                                                        'note= "Upstream
                                                                                                                                                                                                                                note= "Residue from ligation
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                                                               e= "Residue from in construction"
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26-JUN-2002;
21-JAN-2003;
21-JAN-2003;
21-JAN-2003;
21-JAN-2003;
21-JAN-2003;
21-JAN-2003;
       This sequence represents a new vector, pTnMod (Oval/Red)-Chicken, comprising a transposase gene operably linked to a first promoter and one or more gene of interest operably linked to a first promoter promoters, where the one or more genes of interest and their operably linked promoters are flanked by transposase insertion sequences recognized by the transposase and the first promoter comprises a modified Kozak sequence comprising ACCATG. The transposase is a Tn10 transposase and is modified in one to twenty of the first codons. The gene of interest in operably linked to a second promoter, which is a constitutive promoter. The vector further comprises a polya sequence, a conalbumin promoter. The vector further comprises a polya sequence, a conalbumin polya sequence, operably linked to the transposase gene. The vector further comprises a polya sequence gene.
                                                                                                                                                                                                        New vector comprising a transposase gene operably linked to a promoter, useful in treating Alzheimer's disease, breast cancer, phenylketonuria, autoimmune diseases, bacterial or viral infections or Types I and II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                         TRANSGENRES LLC.
UNIV LOUISIANA STATE
                                                                                                                                                                       SEQ ID
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2003US-0441377P.
2003US-0441381P.
2003US-0441392P.
2003US-0441492P.
2003US-0441447P.
2003US-0441447P.
2003US-0441447P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Non-coding lambda
5613. .7477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Multiple
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                                                                                                                                                                     NO 3; 150pp;
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stop codons operably linked to
                                                                                                                                                                                                                                                                                   Fioretti WC,
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC gene. The first or second gene of interest is operably linked to a second CC or third promoter, respectively. The first and a second gene of interest CC are operably linked to a second promoter. The vector further comprises an CC enhancer operably linked to the one or more genes of interest. The CC ventor further comprises at least a portion of an ovalbumin enhancer. The CC ventor further comprises an egg directing sequence, ovalbumin or CC producing stransgenic animals with desired proteins or molecules. They are CC linked to the one or more genes of interest. The vector is useful in CC producing transgenic animals with desired proteins or molecules. They are CC also useful in treating Huntington's disease, alpha-1-antitrypsin CC deficiency, Alzheimer's disease, breast cancer, cystic fibrosis, CC galactosaemia, congenital hypothyroidism, maple syrup urine disease, CC optiz Syndrome, autoimmune diseases, shipping fever in cattle, mastitis, CC bacterial or viral infections or Types I and II diabetes.
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                           IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                               TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
                                                                                                                                                                IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                                                                 MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
                                                                                                                                                                                                                                                                                 AGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGAACCC
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     ATCACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGC
                                                                         TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC
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RESULT 3:
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type; II; diabetes.
                                                                                                                             misc_feature
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/note= "Residue from ligation
used in construction"
133. .1777
                                                                                                                               /*tag= k
/note= "Left insertion
3832. .3837
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/note= "Remainder of F1(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                         /note= "Residue from used in construction" 3838. 4044
                                                                                                                                                                                                                                                                                                                                                                                               'ttag= g
/note= "Residue from ligation of restriction
sed in construction"
2995. .3410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Residue from ligation sed in construction"
                                                                                                                                                                                                                                                                                                                                                      note= "Taken from pGWiz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Two engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Modified
                                                                                                                                                                                                                                                             note= "Non-coding DNA residual from 719. .3761
                                                                                                                                                                                                                 note= "Non-coding lambda DNA
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  "Multiple cloning
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y the a
  pBluescipt11 sk(-)"
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21-JAN-2003;
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                                                                                                                      New vector comprising a transposase gene operably linked to a promoter, useful in treating Alzheimer's disease, breast cancer, phenylketonuria, autoimmune diseases, bacterial or viral infections or Types I and II
                                                                                                                                                                                                                                                                 26-JUN-2002;
21-JAN-2003;
                                                                                                                                                                                                                                                                                           26-JUN-2003; 2003WO-US020389
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                                                                                                                                                                           Cooper RK,
                                                                                                                                                                                           (TRAN-)
                                                                                                                                                                                                                       21-JAN-2003;
                                                                                                                                                                                                                                                                                                            08-JAN-2004.
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                                                                                                                                                                                                                                                          21-JAN-2003;
                                                                                                                                                                                             TRANSGENRES LLC.
UNIV LOUISIANA S
                                                                                                                                                                           Cadd GG,
                                                                                                                                                                                                                      2003US-0441392P.
2003US-0441405P.
2003US-0441447P.
2003US-0441502P.
                                                                                                                                                                                             LOUISIANA STATE & AGRIC & MECH COLL.
                                                                                                                                                                                                                                                                2003US-0441377P
                                                                                                                                                                                                                                                          2003US-0441381P
                                                                                                                                                                                                                                                                           2002US-0392415P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "DsRed reporter coding
from pDsRed1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Multiple cloning site /note= "May be used to insert into the vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in construction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "CMV promoter/enhancer
5694. .5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          into the vector"
4049. .5693
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/note= "Residue from ligation
                                                                                                                                                                                                                                                                                                                                                                note= "Non-coding
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Right insertion sequence
/177. .7218
                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                   note= "Non-coding lambda DNA residual from pNK2859"
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sequence of interest
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This sequence represents a new vector, pTnMod (CMV/Red), comprising a transposase gene operably linked to a first promoter and one or more gene of interest operably linked to one or more additional promoters, where the one or more genes of interest and their operably linked promoters are flanked by transposase insertion sequences recognized by the transposase and the first promoter comprises a modified Kozak sequence comprising ACCATG. The transposase is a Thio transposase and is modified in one to twenty of the first codons. The gene of interest in operably linked to a second promoter, which is a constitutive promoter or an inducible

Example 2; SEQ ID NO 2; 150pp; English

second promoter, which is a constitutive promoter or an promoter, e.g. an ovalbumin or a vitellogenin promoter.

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Percent Similarity:
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further comprises a polyA sequence, a conalbumin polyA sequence, operably linked to the transposase gene. The vector further comprises two stop codons operably linked to the transposase gene. The first or second gene of interest is operably linked to a second or third promoter, second gene cof interest is operably linked to a second or third promoter, second gene cof interest are operably linked to a second promoter. The vector further comprises an enhancer operably linked to the one or more genes of interest. The enhancer comprises at cleast a portion of an ovalbumin enhancer. The vector further comprises an egg directing sequence, ovalbumin or ovomucoid signal sequence or vitellogenin targeting sequence, operably linked to the one or more genes of interest. The vector is useful in producing transgenic animals with desired proteins or molecules. They are also useful in treating completing transpenic animals with desired proteins or molecules. They are also useful in treating that the proteins of disease, alpha-1-antitrypsin deficiency, Alzheimer's compenital hypothyroidism, maple syrup urine disease, neurofibromatosis, phenylketomuria, sickle cell disease, Smith-Lemi-Optiz Syndrome, autoimmune diseases, shipping fever in cattle, mastitis, bacterial or viral infections or Types I and II diabetes.
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IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                  TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp 200
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                                                                             US-10-006-922A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to DNA (I) containing either sequence ABA95905 or sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (PRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum or Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Bacherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern biotechnology. (I) are optimised for expression in yeast and so generate RFP at higher levels with stronger fluorescence and thus lowers the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding red fluorescent protein, useful as marker in biotechnology, has sequence optimized for expression in eukary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana; Escherichia coli; green fluorescent protein; biotechnology; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 681 BP; 198 A; 147
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                                                                                                                                                                                                                                                                                                                                                                                                                          detection limit and gives a better signal-to-noise ratio
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RESULT 41
ABA95907
                                                                                                                                                                                                                        Yeast; red fluorescent protein; RFP; plant; transgenic; GFP; Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana; Escherichia coll; green fluorescent protein; biotechnology; ss.
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(GPCB-) GPC BIOTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACACTGTCAAGTTGAAGGTTACTAAGGGTGGTCCATTGCCATTCGCTTGGGACATCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIleTyr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIle 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCAAGTTCATCGGTGTCAACTTCCCATCTGACGGTCCAGTCATGCAAAAGAAGACTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACAAGAAGTTGTCCTTCCCAGAAGGTTTCAAGTGGGAAAGAGTCATGAACTTCGAAGAGC 306
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> New DNA encoding red fluorescent protein, useful as marker in biotechnology, has sequence optimized for expression in eukaryotes, especially yeast or plants.

Disclosure; Page 11; 19pp; German.

The invention relates to DNA (I) containing either sequence ABA95905 or sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein (VRFP). (I) are used to express red fluorescent protein (RFP) in eukaryotes, especially yeast, especially Saccharomyces cerevisiae and plants, especially dicotyledonous plants including Nicotiana tabacum or Arabidopsis thaliana and also in prokaryotes, especially bacteria, especially Bacherichia coli. RFP is useful in the same way as green fluorescent protein but is more generally applicable in modern biotechnology. (I) are optimised for expression in yeast and so generate RFP at higher levels with stronger fluorescence and thus lowers the detection limit and gives a better signal-to-noise ratio. The present sequence is that of an RNA sequence corresponding to the yeast optimised RFP encoding cDNA given as SEQ ID NO 2 (ABA95906)

Sequence 681 BP; 198 A; 147 C; 161 G; 0 T; 175 U; 0 Other;

D VV	& B &	D Q	D Q	Db Qy	Qγ b	D Qy	US-10-00	Alignment Pred. No.: Score: Percent Si Best Local Query Matc
367 GUCAAGUUCAUCGGUGU 142 GlyTrpGluAlaSerTh 	102 GlyGlyValValThrVal		62 SerProGlnPheGlnTy	42 AsnThrValLysLeuLys	22 ValAsnGlyHisGluPhe             67 GUUAACGGUCACGAAUU	2 ArgSerSerLysAsnVal 	US-10-006-922A-12 (1-225) x ABAS	nent Scores: 9.65e-140 No.: 1209.00 nt Similarity: 100.00% Local Similarity: 100.00% Match: 99.59%
GUCAAGUUCAUCGGUGUCAACUUCCAUCUGACGGUCCAGUCAUGCAAAGAAGAAGACUAUG G1yTrpG1uAlaSerThrG1uArgLeuTyrProArgAspG1yValLeuLysG1yG1uIle 	GlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPholleTyrLys	TyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAsp 	SerProGlnPheGlnTyrGlySerLy8ValTyrValLy8Hi8ProAlaA8pI1eProA8p 	ASNThrVallySLeuLySValThrLySGlyGlyProLeuProPheAlaTrpAspIleLeu 	ValaenglyhisgluphegluilegluglygluglygluglyargProTyrgluglyhis 	<b>≯</b> —н	ABA95907 (1-681)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
JUCAUGCAAAAGAAGACUAUG 426 11 YValleuLygGlyGluIle 161 	AspGlyCysPhGlleTyrLys 121	argValMetAsnPheGluAsp 101 	1isProAlaAspIleProAsp 81                       ACCCAGCUGACAUUCCAGAC 246	ProPheAlaTrpAspIleLeu 61	3lyArgProTyrGluGlyHis 41                    GUAGACCAUACGAAGGUCAC 126	leLysGluPheMetArgPheLysValArgMetGluGlyThr 21 		681 224 0 0

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The invention relates to a fluorescent timer protein having an emission CC spectrum that changes over time after synthesis from a first wavelength CC to a second wavelength. The fluorescent timer proteins are useful in CC monitoring the activity of a promoter, determining the age of a protein, CC identifying an agent that modulates the activity of a promoter and in CC enriching a population of cells comprising a fluorescent timer protein. CC expression during development of a multicellular organism or during CC expression during development of a multicellular organism or during CC expression during intracellular protein movement or translocation, CC promoter activity, as a reporter to serve as a read-out of promoter cC activity, monitoring intracellular protein movement or translocation, CC protein trafficking, or protein stability, to investigate temporal CC aspects of the activity of a regulatory element, for determining cell CC aspects of the activity of a regulatory element, for determining cell CC in distinguishing between newly formed and pre-existing structures, e.g. CC membrane junctions and extracellular matrix components. The fluorescent timer proteins may further be used to investigations where photobleaching techniques are employed, as detectable labels, as selectable markers, as biosensors in protease cleavage assays, and as second messenger detectors. The nucleic acids can be used to generate transgenic, non-human plants or animals or site-specific gene modifications in cell lines. The present sequence is a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, us for monitoring intracellular protein movement, translocation, traffior stability.
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promoter activity; gene expression; transgenic plant; gene modification;
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                                                                                                                                       HisHisLeuPheLeu
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                                                                        standard; cDNA;
                                                                                                                                                                                    IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                                                                                                                                    TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrTyrValAspSerLysLeuAsp
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Anthozoan red fluorescent protein synthetic mutant nucleotide sequence

30-NOV-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a nucleic acid encoding functional red fluorescent (I) that differs from the sequence of an Anthozoan red fluorescent protein by at least one amino acid substitution, and with different fluorescent properties. The red fluorescent protein of the convention can be expressed by standard recombinant methodology. (II) are used a fluorescent markers and FRET partners. It is used for identifying protein-protein interactions. (II) is also suitable for multiplexed protein-protein analysis and FRET-based applications using existing Aequorea fluorescent proteins. (II) has improved brightness, reduced spectral cross talk, and is rapidly and efficiently expressed in mammalian cells. The key mutations in the encoding nucleic acids provide improved folding, brightness, and create (II) with sharper, more defined excitation and emission peaks when expressed in mammalian cells. The present sequence represents the nucleotide sequence of an improved synthetic mutant of an anthozoan fluorescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins for Fluorescence Resonance Energy Transfer (FRET) comprise functional red fluorescent proteins, and the encoding nucleic acids, with key mutations for improving the proteins function.
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GACTACAAGAAGCTGAGCTTCCCCCGAGGGCTTCAAGTGGGAAGAGGGTGATGAACTTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                              LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                                        GACGGCGGCGTGGCGACCCGTGACCCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC 2482
                                                                                                           AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                                    GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                                                   AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                                                                                                                                                                                            CTGTCCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGGCCGACATCCCC
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                                   The invention describes a DNA molecule comprising at least 163 consecutive nucleotide base pairs of the 3' terminal region beginning at the 3' terminal base pair, and at least 125 consecutive nucleotide base pairs of the 5' terminal region beginning at the 5'terminal base pair, of the piggyBac molecule. The region extends from the restriction site SacI to the end of the piggyBac molecule. The DNA molecule in the transposon piggyBac is useful for transferring genes into host cells or embryos for transforming the cells of embryos. The transformed cells or embryos are useful for developing or making transgenic organisms. This sequence represents plasmid used in the creation of minimal sequence eukaryotic
                                                                                                                                                                                                                                 New DNA molecule in the transposon piggyBac, useful for transferring genes into host cells or embryos for transforming the cells of embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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transformed cell; transformed embryo; transgenic; plasmid; cyclic;
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01-NOV-2000;
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                         transformation vector piggyBac
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                                      Alpha-SMA; smooth muscle actin; screening; smooth muscle cell; myofibroblast; gene therapy; red fluorescent protein; ds.
             Synthetic
                                                                             Red fluoroscent protein reporter DNA fragment
                                                                                                         18-SEP-2002
                                                                                                                                 ABL61142;
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This invention describes a novel nucleic acid (I) comprising: (i) at least one functional region (Ia) from the regulatory region of the alphasmooth muscle actin (SMA) gene and (ii) at least one additional functional sequence (Ib) operably linked to (Ia). The products of the invention can be used for preparing genetically modified eukaryotic cells or organisms, for isolation and screening of smooth muscle cells, myofibroblasts or related cells, and for manipulation of gene expression and/or cell function in smooth muscle cell or myofibroblasts or related cells, and for modulation of gene expression and/or cell function in smooth muscle cell or myofibroblasts, particularly for gene therapy. Component (Ia) provides cell-type- or differentiation-specific expression or modulation of genes. This sequence represents a DNA fragment of red fluorescent protein (EGFP) which can be used as a reporter molecule under the control of the alpha-SMA described
                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid containing regulatory region of the smooth muscle actin gene, useful e.g. for manipulating gene expression in smooth muscle
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31-OCT-2000;
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Sequence 666 BP; 202 A; 126 C;
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IleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGlyTrpGlu
                                                ValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysValLysPhe
                                                                                                            LeuSerPheProGluGlyPheLysTrpGluArgValMetAsmPheGluAspGlyGlyVal 104
                                                                                                                                         TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCAGACTATAAAAAAG
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The invention describes a first mutant fluorescent protein (I) comprising an amino acid sequence that differs from that of a corresponding wild-type red fluorescent protein by an amino acid substitution, where the
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The invention describes a first mutant fluorescent protein (I) comprising CC an amino acid sequence that differs from that of a corresponding wild-crype red fluorescent protein by an amino acid substitution, where the CC differs mutation fluorescent protein mutant has an optical property that CC differs relative to the corresponding optical property produced by the CC wild-type red or green fluorescent protein. (I) is useful for detecting expression of gene. The polynucleotide (II) encoding (I) is useful for CC expression of gene. The polynucleotide (II) encoding (I) into a CC cell or organism, allowing the cell to replicate, and detecting expression of the nucleic acid by emission of fluorescent light. The CC expression of the nucleic acid expression is detected in vivo or in CC vitro. (II) is useful for regenerating an animal such as zebrafish CC which contains (II). (I) is useful as a marker for detecting expression of a gene, in biochemical assesys, and as reagents. (I) is also useful in manual such as in manual such as in manual contains of genetics, as in vivo markers such as in manual such as in manual contains.)
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mutant RedII"
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The invention relates to mutant red and green fluorescent proteins which they higher fluorescent intensities compared to the wild-type proteins of from which they are derived. The invention also discloses nucleic acids encoding the mutant fluorescent proteins, and transgenic animals of the invention, Red I (ADZ84223) and Red II (ADZ84225), are derived from a novel wild-type RFP (referred to as Ac/DBRP) isolated from a comparising such a nucleic acid. The mutant red fluorescent proteins (RFP) of the invention, Red I (ADZ84223) and Red II (ADZ84225), are derived from a novel wild-type RFP (referred to as Ac/DBRP) isolated from a compared to be either an Actinodiscus or Discosoma (C (ADZ84227)) and Green (ADZ84229), are derived from a novel wild-type GFP (Rnown as McGFP) isolated from the great star coral Montastraea covernosa. The Ac/DBRPP and McGFP mutants were obtained by subjecting the wild-type Ac/DBRPP and McGFP cDNAs to low-stringency PCR to introduce covertors, and selecting the transformed bacteria having higher relative fluorescence compared to those expressing the wild-type proteins. The compared to those expressing the wild-type proteins. The compared to those expressing the wild-type proteins. The coral proteins of the invention may be used in a wide range of agene of interest, or can be used as markers for detecting the expression can general proteins, or can be used as in vivo markers in multiple capression systems (e.g., as components of fusion proteins), in multiple colored food additives and as color indicators in diagnostic kits, as colored cordarian genetics, as color indicators in diagnostic kits, as colored cordarian genetics, as color indicators in diagnostic kits, as colored cordarian sentence of the mutant Actinodiscus/Discosoma red fluorescent cordarian sentence of the mutant 
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(CART/) CARTER R W.
(SCHM/) SCHMALE M C.
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US-10-006-922A-12 (1-225) x ADZ84224 (1-711)

MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly

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61 21

ACGGTCAATGGGCACGAGTTTGAAATAGAAGGCGAAGGAGAAGGGAGGCCATACGAAGGC ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly

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The invention relates to mutant red and green fluorescent proteins which they are derived. The invention also discloses nucleic acids encoding the mutant fluorescent proteins, and transgenic animals comprising such a nucleic acid. The mutant red fluorescent proteins (RFP) of the invention, Red I (ADZ84223) and Red II (ADZ84225), are derived from a novel wild-type RFP (referred to as Ac/DBRFP) isolated from a gencies, while the mutant green fluorescent proteins (RFP) (RDZ84227) and Green (ADZ84223), are derived from a novel wild-type RFP (referred to as Ac/DBRFP) isolated from a gencies, while the mutant green fluorescent proteins (GFP), Green I (CADZ84227) and Green (ADZ84229), are derived from a novel wild-type GFP (Known as MGGFP) isolated from the great star coral Montastraea (CADZ84227) and GFPP and MGGFP cDNAs to low-stringency PCR to introduce vectors, and selecting the PCR products into bacterial expression core fluorescence compared to those expressing the wild-type proteins. The mutant fluorescent proteins of the invention may be used in a wide range of a gene of interest, or can be used as in vivo markers in mRNA (CADZ8423) are useful as markers for detecting the expression of a gene of interest, or can be used as in vivo markers in mRNA (CADZ8425) as color indicators in diagnostic kits, as colored food additionally be used as taxonomic markers for studies of condardistives and as cosmetic ingredients. They present sequence (CADZ8425) as color indicators in diagnostic kits, as colored food additives and as cosmetic ingredients. The present sequence (CADZ8425) as color indicators in diagnostic kits, as colored to mote mutant Actinodiscus/Discosoma red fluorescent protein Red II. Red II was found to have a fluorescent intensity at least to the mutant RFP Red I (ADZ8423).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel mutant fluorescent protein comprising amino acid sequence that differs from wild-type red or green fluorescent protein by amino acid substitutions, useful as markers for detecting desired gene expression.
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(CART/) CARTER R W.
(SCHM/) SCHMALE M C.
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DB; ADZ84225.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Mutant Ac/DeRFP Red replace(694,G)
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Percent Similarity: Best Local Similarity: Query Match:

4.18e-138 1196.00 99.11% 98.22% 98.52%

Matches: Conservative: Mismatches: Indels: Gaps:

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RESULT 51
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                                                                                                           Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; NFP-6; gene;
                                                    Discosoma sp. Synthetic.
                                                                                                                                                                                                Discosoma sp. drFP583 (NFP-6) mutant DNA,
                                                                                                                                                                                                                             27-DEC-2002
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                                                                                                mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) mutant DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a non-aggregating chromo-
of an aggregating Cnidarian chromo- or fluorescent p
analyte detection assays or fluorescence activated c
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04-DEC-2001;
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                                                                 AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
                                                                                              GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                                                  LeuSerProGlnPheGlnTyrGlySerLy8ValTyrValLy8Hi8ProAlaAspIlePro
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                                                                                                                                                                                                                                                                            ThrValAsmGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
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The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer proteins are useful in monitoring the activity of a promoter, determining the age of a protein, identifying an agent that modulates the activity of a promoter and in enriching a population of cells comprising a fluorescent timer protein. The fluorescent timer protein are also useful for assessing gene
                                                                                                                                                                                                                                                                                                New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking
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cc expression during development of a multicellular organism or during cellular differentiation, in response to a drug or other inducer of component activity, as a reporter to serve as a read-out of promoter cc activity, monitoring intracellular protein movement or translocation, cc protein trafficking, or protein stability, to investigate temporal cc aspects of the activity of a regulatory element, for determining cell cf fate during development and organ remodelling, in spatial and temporal cc in distinguishing between newly formed and pre-existing structures, e.g. membrane junctions and extracellular matrix components. The fluorescent timer proteins may further be used to investigations where photoblacking techniques are employed, as detectable labels, as selectable markers, as biosensors in prokaryotic and eukaryotic cells, in protease cleavage cc assays, and as second messenger detectors. The nucleic acids can be used to generate transgenic, non-human plants or animals or site-specific gene modifications in cell lines. The present sequence is a cDNA encoding CC Discosoma sp. ESNA non-aggregating fluorescent timer protein derived from fluorescent timer protein derived from humanised wild-type Anthozoa CC R2A, K2E and K9T. E5 protein is derived from humanised wild-type Anthozoa CC protein drf9583 by substituting Val to Ala at 105 and Ser to Thr at 197 XX
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                                                 The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) mutant DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                   of an aggregating analyte detection
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        BP;
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2001US-00006922.
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/note= "No stop codon"
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23-DEC-2004
                               US2004261149-A1
                                                                                          gene silencing; plant; short interfering RNA; siRNA; RNA interference;
phage resistance; ds; gene; dsRed.
                                                                                                                                       Plant cell gene silencing related dsRed gene coding region.
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                                                                                                                                                                                                                                                                                                                                                                                               US-10-006-922A-12 (1-225) x ADV96699 (1-747)
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) PADMANABHAN C.
) RAMACHANDRAN V.
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                                                                                                                                           CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGGCCGACATCCCC
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This sequence represents the construct UbCP-lox-mirMSOD2-EGFP-lox-RFP. In this construct, the Ubiquitin C promoter (UbCP) normally directs synthesis of the hairpin and EGFP. However, upon exposure to cre, the hairpin and EGFP re excised thus preventing hairpin expression, while the RFP gene is under the control of the UbCP. This sequence is a complementary vector to UbCP-lox-RFP-lox-mirMSOD2-EGFP. The construct of the invention comprises a U6 promoter operably linked to a shRNA encoding nucleic acid sequence. The construct further comprises a first loxP site upstream of the promoter and a second loxP site same orientation so that the promoter and encoding sequence, the loxP sites are in the same orientation so that the shRNA encoding sequence comprises a first stem-encoding portion, a loop-encoding portion, and a second stem-encoding portion, the loop-encoding portion a first loxP site operably linked to a transcription
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gain-of-function mutation; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO 9; 88pp; English
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cc termination signal upstream of a spacer DNA and a second loxP site, the CC loxP sites are in the same orientation so that the first loxP site, the construct further comprises spacer DNA are excisable upon exposure to Cre. The construct further comprises spacer DNA downstream of the shRNA encoding sequence, a second loxP site downstream of the shRNA encoding cc sequence, the loxP sites are in the same orientation so that the spacer DNA and second stem-encoding sequence are excisable upon exposure to Cre. The U6 promoter comprises a distal sequence element (DSE), a proximal cc sequence element (PSE), and a TNTA box, operably linked, where the construct comprises a first loxP site downstream of the shRNA encoding equence, and a second loxP site between the DSE and the PSE, the loxP cc sites are in the same orientation so that the shRNA encoding cc sequence, and a second loxP site between the DSE and the TATA box are cc excisable upon exposure to Cre. The construct also comprises a first loxP site and a second loxP site, the sites are interrupted by spacer DNA, cc site and a second loxP site, the sites are interrupted by spacer DNA, between the DSE and the PSE, the loxP sites are in the same orientation so that the same orientation cc cre. The construct is useful for the treatment of a disease, which is caused by aberrant gene function. The disease is a dominant, gain-of-function, both physiologic and pathologic, in specific cell groups and cc in specific ages, in normal and diseased pathways. 

Sequence 4200 BP; 889 A; 1094 C; 1265 G; 950 T; 0 U; 2 Other

Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-10-006-922A-12 (1-225) x ADW43589 (1-4200) Score: No.: 8.85e-136 1186.00 98.22% 97.33% 97.69% Conservative: Mismatches: Indels: Length: Matches: Gaps:

밁 8 δ 밁 δ 밁 Ś 밁 5 S 밁 S 밁 Ś 밁 र् 밁 밁 3627 3567 3507 3447 3387 3327 141 121 101 81 61 41 21 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40 MetArgSerSerLy8AsnVallleLysGluPheMetArgPheLy8ValArgMetGluGly 20 HisasnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTTpAspIle 60 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180 AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTGATGCAGAAGAAGACC LysValLysPheI1eGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140 GACGGCGGCGTGGCGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120 GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100 LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80 CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGCCCCTGCCCTTCGCCTTGGGACATC 3446 ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCCCTACGAGGGC 3386 ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCCGAG CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC 3746 160 3686 3626 3566 3506 3806

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RESULT 56
ADW43588
ID ADW4588
This sequence represents the construct UbCP-lox-RFP-lox-mirMSOD2-EGFP. In this construct, the Ubiquitin C promoter (UbCP) normally transcribes RFP CC mRNA, which terminates at a polyA site. However, because the RFP gene is construct to loxe sites, upon exposure to cre, the RFP gene is excised and the construct is converted to UbCP-lox-mirMSOD2-EGFP. The resulting CC construct of the invention comprises a message that contains an intron with an CC shRNA (small hairpin) against the mouse SOD2 gene and an EGFP gene. The CC construct of the invention comprises a U6 promoter operably linked to a Cfirst loxe site upstream of the promoter and a second loxe site upstream of the promoter and a second loxe site the construct further comprises a CC downstream of the promoter and encoding sequences are in the same CC exposure to Cre. The shRNA encoding sequence, the loxe sites are in the same CC upon exposure to Cre. The shRNA encoding sequence sare excisable constrion, the loop-encoding portion comprising a first loxe site operably linked to a transcription termination signal upstream of a spacer DNA and second loxe site, the loxe sites are in the same orientation so that the loxe site, termination signal and spacer DNA are excisable upon exposure to Cre. The construct further comprises spacer DNA downstream of the spacer DNA, and a first loxe site within the loop-encoding portion of the shRNA encoding sequence, a second loxe site downstream of the spacer DNA and sequence, the loxe sites are in the same orientation so that the spacer DNA and second stem-encoding sequence are excisable upon exposure to Cre. The U6 promoter comprises a distal sequence element (DSB), a proximal sequence element (DSB), a and a TATA box, operably linked, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New construct comprises a U6 promoter operably linked to a small hairpin RNA (shRNA) encoding nucleic acid sequence, useful for regulating shRNA expression in cells or animals.
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문 S 밁 S 밁 S 밁 á 밁 δ 밁 δ 밁 S 밁 S 문 5 밁 S 밁 Ś US-10-006-922A-12 (1-225) x ADW43588 (1-4300) Query Match: DB: Percent Similarity: Best Local Similarity: CC encoding sequence, and a second loxP site downstream of the shRNA CC encoding sequence, and a second loxP site between the DSE and the PSE, CC the loxP sites are in the same orientation so that the shRNA encoding CC sequences and a portion of the promoter comprising the PSE and the TATA CC box are excisable upon exposure to Cre. The construct also comprises a CC first loxP site and a second loxP site, the sites are interrupted by CC spacer DNA, between the DSE and the PSE, the loxP sites are in the same CC exposure to Cre. The construct is useful for the treatment of a disease, CC which is caused by aberrant gene function. The disease is a dominant, CC gain-of-function mutation, e.g. a neurological disease is a dominant, CC constructs methods, kits, and compositions are useful for investigating CC constructs, both physiologic and pathologic, in specific cell groups CC and in specific ages, in normal and diseased pathways. Sequence 4300 BP; 906 A; 1128 C; 1297 G; 967 T; 0 U; 2 Other; 1591 1471 1651 1411 1351 ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCC 1291 ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC 1771 ACCCACAAGGCCCTGAAGCTGAAGGACGGCCGCCACTACCTGGTGGAGTTCAAGTCCATC 141 101 61 21 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40 IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTGATGCAGAAGAAGAACC 1710 LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120 AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100 LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro HisasnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly GACGGCGGCGTGGCGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC 1650 CTGTCCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATC TACATEGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACGCCAAGCTGGAC ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG 9.15e-136 1186.00 98.22% 97.33% 97.69% Length: Matches: Gaps: Mismatches: Indels: Conservative: 220 180 1770 160 140 1590 1470 1410 1350 1890 200 1830 1530 80 60 20

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CC preparation of a recombinant vector comprising a heterologous gene cc sequence such as an anti-apoptotic gene e.g. bcl-2 or PTEN, a determination/differentiation gene such as the dopaminergic determination determination factor Nurri, a gene capable of inducing neuronal migration e.g. cc neurophilin or SDF-1 or a transcription factor gene such as NeuroD or CC BMP4. The present invention describes non-human transgenic animals that cc have been transfected with such a vector that can be used for screening compounds in vitro to identify those with neurogenic properties capable of regulating neural stem cell activity, neurogenesis and/or neuronal cc differentiation, which can subsequently be used in the development of capacity of the pharmaceutical compositions. Furthermore, these transgenic can mails can be used for the in vivo tracking of newly generated neurons, can swell as for transplanted or migrating neuronal determined cells. Cc neurological disorders e.g. epilepsy or stroke and for the enhancement of clasming and/or memory skills caused by neurodegenerative disorders such cas parkinson's, Huntington's or HIV-dementia, as well as psychiatric cor brain malformation. Hence, these compositions exhibit vasotropic, can toornvulsant, cerebroprotective, antiparkinsonian, neuroprotective, conoctropic and anti-HIV activities. This polynucleotide sequence is the fusion construct DNA of the reporter gene DSRed2 under the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTEN; dopaminergic determination factor; Nurri; neuronal migration; neurophilin; SDF-1; NeuroD; BMP4; transgenic; neurogenic; neurolgical disorder; epilepsy; stroke; learning; memory skill; neurodegenerative disorder; Parkinson's; Huntington's; HIV-dementia; psychiatric disorder; tumourous disorder; brain malformation; vasotropic; anticonvulsant; cerebroprotective; antiparkinsonian; neuroprotective; nootropic; anti-HIV; regulatory sequence; proliferative neuronal determined cell; anti-apoptotic.
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Plasmid pLL3.2 nucleotide sequence

SEQ ID NO:4.

lentiviral vector; functional packaging signal; multiple cloning site; antimicrobial; gene therapy; infection; plasmid; pLL3.2; circular; gene;

gene

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The present invention describes a lentiviral vector comprising a nucleic acid whose sequence includes a functional packaging signal, a multiple cloning site (MCS), and at least one additional element selected from a second MCS, a second MCS into which a heterologous nucleic acid is inserted, an HIV FLAP element, an expression-enhancing posttranscriptional regulatory element, a target site for a site-specific recombinase, and a self-inactivating (SIN) LTR. Also described: (1) a lentiviral vector comprising the RNA polymerase III promoter; (2) a collection of at least two lentiviral vectors; (3) a three plasmid
                                                                                                                                    New lentiviral vector comprising a nucleic acid whose sequence includes a functional packaging signal, a multiple cloning site (MCS), and at least one additional element, useful for treating infectious diseases.
                                                                                                                                                                                                                                                    06-SEP-2002; 2002US-0408558P.
27-SEP-2002; 2002US-0414195P.
21-NOV-2002; 2002US-0428039P.
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/note= "LoxP"
3594. .4183
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5713. .6573
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422. .2599
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CC lentiviral expression system; (4) a four plasmid lentiviral expression CC comprising the three plasmid lentiviral expression system, further CC comprising a four plasmid comprising a nucleic acid sequence that encodes CC Rev, operably linked to a promoter; (5) a cell comprising the lentiviral CC vector; (7) a transgenic animal, at least some of whose cells contain a CC provirus derived from the lentiviral vector; (8) a method of creating a provirus derived from the lentiviral vector; (8) a method of creating a provirus derived from the lentiviral vector; (8) a method of creating a provirus derived from the lentiviral vector; (8) a method of creating a provirus derived from the lentiviral vector; (8) a method of producing lentiviral particles; (10) a method for achieving controlled expression of a heterologous nucleic caid in a cell; (12) a method for expression of a heterologous nucleic cell type or tissue-specific manner; (13) a composition comprising the contiviral vector and a carrier; (15) methods of reversibly inhibiting or reducing expression of a hearyest transcript in a cell, or in a mammal in a cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner; (16) a method of treating or cell type or tissue-specific manner.
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                      IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                                                                                                         LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                                                                                                                   AspG1yG1yVa1Va1ThrVa1ThrG1nAspSerSerLeuG1nAspG1yCysPheI1eTyr
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ACCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
                                                                         MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
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29-NOV-2002; 2002US-00306737.
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1777. .1804
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'note= "Vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid construct useful for screening substances for their ability to influence production of brain derived neurotrophic factor (BDNF), comprises promoter of BDNF gene and red fluorescent reporter.
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                                                                              | IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
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                       CC BMP4. The present invention describes non-human transgenic animals that CC have been transfected with such a vector that can be used for screening CC compounds in vitro to identify those with neurogenic properties capable of regulating neural stem cell activity, neurogenesis and/or neuronal CC differentiation, which can subsequently be used in the development of CC appropriate pharmaceutical compositions. Furthermore, these transgenic CC animals can be used for the in vivo tracking of newly generated neurons, CC as well as for transplanted or migrating neuronal determined cells.

CC Accordingly, such compositions can be used in gene therapy for CC neurological disorders e.g. epilepsy or stroke and for the enhancement of CC neurological disorders e.g. epilepsy or stroke and for the enhancement of CC as Parkinson's, Huntington's or HIV-dementia, as well as psychiatric CC disorders, tumourous disorders of the nervous system or a developmental CC or brain malformation. Hence, these compositions exhibit vasotropic, CC anticonvulsant, cerebroprotective, antiparkinsonian, neuroprotective, conception vector phubCxpromobSRedZ, which comprises the reporter gene conception of the newly service and the reporter gene conception to the control of the human reservations.
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Synthetic.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to the novel use of regulatory sequences for the early, translant expression of a heterologous nucleotide sequences in proliferative neuronal determined cells. Specifically, it refers to the preparation of a recombinant vector comprising a heterologous gene sequence such as an anti-apoptotic gene e.g. bcl-2 or PTEN, a determination/differentiation gene such as the doppaminergic determination factor Nurrl, a gene capable of inducing neuronal migration e.g. neurophilin or SDF-1 or a transcription factor gene such as Neurophile that
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lentiviral vector; functional packaging signal; multiple cloning site;

antimicrobial;

gene therapy; infection; plasmid; pLL3.5; circular; gene;

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06-SEP-2002;
27-SEP-2002;
21-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
The present invention describes a lentiviral vector comprising a nucleic acid whose sequence includes a functional packaging signal, a multiple cloning site (MCS), and at least one additional element selected from a second MCS, a second MCS into which a heterologous nucleic acid is inserted, an HIV FLAP element, an expression-enhancing posttranscriptional regulatory element, a target site for a site-specific recombinase, and a self-inactivating (SIN) LTR. Also described: (1) a
                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus
                                                                                                      New lentiviral vector comprising a nucleic acid whose sequence includes a functional packaging signal, a multiple cloning site (MCS), and at least one additional element, useful for treating infectious diseases.
                                                                                                                                                                                                                                                       05-SEP-2003; 2003WO-US028111.
                                                                                                                                                  WPI; 2004-315566/29.
                                                                                                                                                                                                                                                                              18-MAR-2004
                                                                                                                                                                                                                                                                                                  WO2004022722-A2.
                                                                                                                                                                                                                                                                                                                                                                        rep_origin
                                                                                                                                                                                          (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                      Ä,
                                                                                  43, SEQ ID NO 7; 197pp; English.
                                                                                                                                                                      Dillon CP,
                                                                                                                                                                                                              2002US-0408558P.
2002US-0414195P.
2002US-0428039P.
                                                                                                                                                                                                                                                                                                                                        /note= "pUC"
6934. .7794
                                                                                                                                                                                                                                                                                                                                            6934.
                                                                                                                                                                                                                                                                                                                                                                                   note= "3' SIN LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "HIV RRE (HIV NL4-3/7622-8459)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                      product= "AmpR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "dsRed2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "5' HIV R-U5-del gag (HIV NL4-3/454-1126)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "CMV promoter/enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                   note= "WRE element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                notes "LoxP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "UbC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "LoxP"
993. .4673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727. .4760
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                                                                                                                                                                      Rubinson DA, Van Parijs L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flap"
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CC collection of at least two lentiviral vectors; (3) a three plasmid CC collection of at least two lentiviral vectors; (3) a three plasmid CC lentiviral expression system; (4) a four plasmid lentiviral expression CC system comprising the three plasmid lentiviral expression system, further comprising a four plasmid comprising a nucleic acid sequence that encodes CC Rev, operably linked to a promoter; (5) a cell comprising the lentiviral vector; (6) a cell comprising a provirus derived from the lentiviral CC vector; (7) a transgenic animal, at least some of whose cells contain a CC producer cell line; (9) a method of producing lentiviral vector; (8) a method for achieving controlled expression of a heterologous nucleic acid in a target cell; (11) CC a method for achieving controlled expression of a heterologous nucleic cell type or tissue-specific manner; (13) a composition comprising the CC lentiviral vector, and a delivery agent that enhances delivery of the CC lentiviral vector and a carrier; (15) methods of reversibly inhibiting or CC cell type or tissue-specific manner; (16) a method of treating the CC condition; and (17) a kit comprising the lentiviral vector and a carrier; (16) a method of treating or CC preventing infection by an infectious agent, or a disease or clinical CC condition; and (17) a kit comprising the lentiviral transfer plasmid and CC can be used in gene therapy. The lentiviral vector, compositions and cCC exemplification of the plasmid plias. 5 nucleotide sequence, which is used in the CCC exemplification of the present invention.
exemplification of the present invention.
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Sequence 7927 BP; 1958 A; 1925 ü 2151 G; 1893 T; 0 U; 0 Other;

Best Local Similarity: Query Match: DB:

Percent Similarity:

2.17e-135 1186.00 98.22% 97.33% 97.69%

Mismatches: Conservative: Indels:

Pred.

Score:

Alignment Scores:

US-10-0	10-006-922A-12 (1-225) x ADL35211 (1-7927)	
Ş	1 MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly 20	
<b>B</b>	3999 ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC 4058	
8	21 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40	
망	4059 ACCGTGAACGGCCACGAGTTCGAGGTCGAGGGCGAGGGCCGCCCCTACGAGGGC 4118	
Ş	41 HisasnThrVallysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60	
망	4119 CACAACACCGTGAAGGTGAACGAAGGGCGGCCCCTGCCCTTCGCCTTGGGACATC 4178	
Ş	61 LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80	
뭥	4179 CTGTCCCCCCAGTTCCAGTACGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC 4238	
Ś	81 AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMctAsnPheGlu 100	
망	4239 GACTACAAGAAGCTGTCCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG 4298	
ঠ	101 AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120	
망	4299 GACGGCGTGGCGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC 4358	
\$	121 LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140	
DЬ	4359 AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTGATGCAGAAGAAGACC 4418	
Ą	141 MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160	
дb	4419 ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG 4478	
8	161 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180	

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ADMINIT 65
ADMINIT 65
ADMINIT 10

Alignment Scores:
                                                                                                                                The invention relates to a novel method for screening for inducers or combibitors of a DNA repair pathway by contacting at least one component of a DNA repair pathway with a non-circularized retroviral cDNA in the presence and absence of a test compound, and determining whether circularization of the cDNA is increased or decreased in the presence of the test compound. The DNA repair pathway components have the following continuities anti-HIV, cytostatic, virucide, antidiabetic, and condulate a DNA repair pathway and/or retroviral activity. The compound is useful for identifying compounds that consolidate a DNA repair pathway and/or retroviral activity. The compound is useful in manufacturing a pharmaceutical composition for the treatment of a crtroviral infection (e.g. AIDS, HIV infection, cancer, human adult T-cc cell leukaemia, lymphoma, feline immundeficiency virus, Type I diabetes or multiple sclerosis) or for increasing the efficiency of gene delivery cin a gene therapy. This polynucleotide represents a retroviral cDNA consolidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for compounds that modulate a DNA repair pathway and/or retroviral integration, useful for treating retroviral infection, comprises determining the amount of a retroviral cDNA circularization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inducer; inhibitor; DNA repair pathway; anti-HIV; cytostatic; virucide; antidiabetic; neuroprotective; retroval; infection; AIDS; HIV infection; cancer; human adult T-cell leukaemia; lymphoma; feline immunodeficiency virus; Type I diabetes; multiple sclerosis;
                                                                         Sequence 9731 BP; 2444 A; 2412 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 73; SEQ ID NO 5; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-854096/79.
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Best Local Similarity:
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                                                              antidiabetic; neuroprotective; retroviral infection; AIDS; HIV infectioner; human adult T-cell leukaemia; lymphoma; feline immunodeficiency virus; Type I diabetes; multiple sclerosis;
                               gene therapy; human; cyclic;
                                                                                                                                    inducer; inhibitor; DNA repair pathway; anti-HIV; cytostatic; v
antidiabetic; neuroprotective; retroviral infection; AIDS; HIV
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                                                                                                                                                                                                                                  DNA repair
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AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                            AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
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                    Novel fluorescent protein from non-bioluminescent Discosoma useful for fluorescent labeling and as markers.
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14-OCT-1999;
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/transl_except= (pos:456. .457, aa:Val)
/transl_except= (pos:470. .473, aa:Val)
/transl_except= (pos:470. .473, aa:Val)
/note= "The codon at position 456. .457 has an apparent incleotide deletion which alters the reading frame. The codon at position 470. .473 has an apparent 1 nucleotide insertion which corrects the altered reading frame"
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Claim 6; Page 73-74; 86pp; English

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IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                     TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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                                                                                                                                                                                              ATTCATAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAAGTATT
                                                                                                                                                                                                                                     IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTCAAGTTCATTGGCGTTGAACTTTCCTTCCGATGGACCTGTTATGCAAAAGAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGGTGGCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTAC
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The present sequence is a Discosoma sp. red chromo/fluorescent protein, drFP583 (NFP-6) cDNA. NFP-6 is present in an environment other than its natural environment and has an absorbance maximum ranging from 250nm to

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RASULT 65
AADO3615
ID AADO3
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14-JUN-2000;
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14-JUN-2000;
14-JUN-2000;
                                                                                                                                                                An Anthozoa chromo- or fluorescent protein (P1) present in an environment other than its natural environment, useful as a label in analyte detection assays and as a selectable marker in recombinant DNA
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09-DEC-1999
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19-JUN-2001
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15-OCT-1999;
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DB; AAE00375.
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                                                                                                                                                                                                                                                                                                                                                                                    CLONTECH LAB
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                                                                                             Fig 6; 69pp; English.
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2000US-0211607P
2000US-0211626P
2000US-0211626P
2000US-0211627P
2000US-0211687P
2000US-0211766P
2000US-021188P
2000US-0211888P
2000US-0211888P
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99US-00458144.
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/product= "Chromo/fluorescent protein, drFP583 (NFP-6)"
/transl_except= (pos:540. .600, aa:Leu-Gly)
/note= "Insertion of 60 bases alters the reading frame"
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                                                                                                                                                                                                                                                                                                                                     Labas YA,
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Percent Similarity:
Best Local Similarity:
Query Match:
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ADC24128
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                                                                                                                            HisHisLeuPheLeu
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                                                                                                                                                                                                                                                                                                                                                  IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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ADC24128 standard;

DNA; 678

Percent Similarity: Best Local Similarity:

1160.00 97.33% 96.00%

Length:
Matches:
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CC Discosoma red fluorescent protein (DsRed) variant having a reduced CC Discosoma red fluorescent protein (DsRed) variant having a reduced CC and/or AC interfaces of the wild-type DsRed sequence (SI) comprising 225 CC and/or AC interfaces of the wild-type DsRed sequence (SI) comprising 225 CC amino acids, given in the specification, where the substitutions at the AB CC conatining a vector which comprises (I) operatively linked to an CC conatining a vector which comprises (I) operatively linked to an CC expression control sequence, and an unit to assay the variant fluorescent grotein fluorescence, and assaying fluorescence of the variant fluorescent protein produced by (VII), where variant fluorescent protein fluorescence is indicative of transcriptional activity. A polymucleotide comprises is useful for the analysis of in vivo concent protein produced, where the target protein admount of a carget protein produced, where the target protein and amount of a carget protein produced, where the target protein is fused to the marker, as a complement to or alternative for the green fluorescent protein or its spectral variant, for detecting induction of transcriptions, in capplications involving fluorescence energy resonance transfer (PRET), capplications and acceptors towards or away from each other, for making fluorescent sensors for protein kinase and phosphatase activities or indicators for ions and molecules such as Cal., Znl., for identifying the protein as asmple, for identifying a specific consecut for identifying a region or condition that regulates the activity useful contains an enzyme or for determining the plu of the sample. (I) is useful for identifying a region or condition that regulates the activity of an expression control sequence. This sequence encodes Discosoma red control of a first and second molecule, for determining the plus of the activity of the control of the movement of the activity of the protein protein variant fast Tl.
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                                                                                                          Discosoma
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oligomerization; tetramerization; immunoassay; hybridization assay.
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The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful molecular biology, e.g. in immunoassays or in tracking protein
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29-JUL-2002; 2002US-00209208
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                                                                         coding sequence for the variant
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1.13e-133 1160.00 97.33% 96.00% 95.55% Length: Matches: Conservative: Mismatches: 678 216 0

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AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
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ID ADN333
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XX D193
XX O1-JU
XX Chida
KW Mutan
XX D190
PN W0200
XX H0200
XX
The present invention relates to nucleic acid that encodes a rapidly maturing chromo or fluorescent mutant of a Chidarian chromo- or fluorescent protein or its mutant. The protein is useful in applications involving nucleic acid encoding a chromo- or fluorescent protein and is useful for producing a chromo and/or fluorescent protein which involves growing the cell, whereby the protein is expressed, and isolating the protein substantially free of other proteins. The protein is useful in applications involving chromo- or fluorescent protein and is useful as pclications involving chromo- or fluorescent protein and is useful as pcR primers, hybridization probes, etc. The expression cassettes are useful for synthesizing related proteins. The chromoproteins are useful as coloring agents which are capable of imparting color or pigment to a particular composition which are capable of imparting color or pigment to a particular composition which are capable of imparting color or passettes in an adjusted effection assays, e.g. assays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid encoding a rapidly maturing chromo- or fluorescent mutant of a Cnidarian chromo- or fluorescent protein or its mutant, useful for applications involving chromo- or fluorescent proteins.
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                                                                                                                                                                biological analytes of interest and as selectable markers in recombinant DNA applications, e.g. the production of transgenic cells and organisms. The fluorescent proteins find use in a variety of different applications, e.g. in fluorescence resonance energy transfer (FRET) applications in prokaryotic and eukaryotic cells, in applications involving the automated screening of arrays of cells expressing fluorescent reporting groups by using microscopic imaging and electronic analysis, as second messenger detectors, and in fluorescence activated cell sorting applications and as in vivo marker in animals. The fluorescent proteins also find use in protease cleavage assays. The proteins can also be used is assays to determine the phospholipid composition in biological membranes and as a fluorescent timer. The present sequence represents the mutant-type DBRED encoding sequence.
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Sequence 704 BP; 145 A; 237 C; 212 G; 110 T; 0 U; 0 Other;

Length: Matches:

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Alignment Scores: Pred. No.:

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HisHisLeuPheLeu 225
                                             IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                       TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrTyrValAspSerLysLeuAsp
                                                                                                                                    IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                       ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
                                                                                                                                                                                                                  GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                           TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGAC
                                                                                                                        ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
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RESULT 69
ADM13536
ID ADM13536
AC ADM13
CC The invention relates to a green fluorescent protein (GFP) that comprises CC at least 80% identity to the GFP superfolding mutant appearing as CC ADM13335 that has at least one amino acid substitution selected from CC e.g., a substitution at position 30 that is an arginine or a conservative CC variant of arginine and measurable fluorescence activity. Also included CC are directed-evolution for generating an enhanced folding variant of a CC polypeptide (comprising mutating applymucleotide encoding CC polypeptide of interest to generate a library of mutated polymucleotides, CC linking mutated polymucleotides to polymucleotide encoding folding interference domain to form fusion protein (FP) constructs, expressing CC PP, and selecting FP that display optimal folding activity in relation to FP comprising wild-type polypeptide and folding activity in relation to FP comprising variant of a fluorescent protein generated by the method, an cenhanced folding variant of a fluorescent protein generated by the method, an cenhanced folding variant of a chromophoric protein generated by the CC introduced folding variant of a chromophoric protein generated by the constitution of the polypeptide to a poorly folding CC domain, to form a fusion protein, mutating the first domain, detecting an CC increase in the amount of activity generated by a first mutated fusion protein in comparison to a fusion protein comprising a wild-type first CC domain and the poorly folding, joining a second domain, thus identifying a comparison to a fusion protein comprising the wild-type second domain and created by a first mutated fusion protein motorial material mutated fusion protein comprising the wild-type second domain and the poorly folding, joining a second domain and the created fusion protein comprising the wild-type second domain and creativity generated by a second domain for the mutated fusion protein comprising the wild-type second domain and creativity generated by a second domain protein according to the mutated fusion protein compri
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directed-evolution; folding interference domain; reporter protein;
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RESULT 70 ADC24130

standard; DNA;

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Discosoma red fluorescent protein variant dimer2 DNA

ADC24130 sta ADC24130; 18-DEC-2003

(first entry)

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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DsRed enhanced folding variant. NOTE: The authors refer to as SEQ ID 1-5 throughout the specification and never refer by number, it is obvious that SEQ ID 38-42 are meant to be
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                  HisHisLeuPheLeu
                                                                                                                                                                                    IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                                                                 MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                                                                                                    LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                                                                                                                                                                                                                                                         AspG1yG1yVa1Va1ThrVa1ThrG1nAspSerSerLeuG1nAspG1yCysPheI1eTyr
                                                                                                                                                                                                                                                                                                                                                                                             AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
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  CACCATCTGTTCCTT
                                                                     | IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                          TACATGGCAAAGAAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAAACTGGAT
                                                                                                                         TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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                                                                                                                                                                                                                                                                                                                          GACGGTGGCGTCGCTACTGTAACCCAGGATTCCAGTTTGGAGGATGGCTGTTTGATCTAC
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                                                      ATAACAAACCACAACGAAGACTATACAATCGTTGAGCAGTATGAAAGAGCCGAGGGACGC
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CC The invention describes a polynucleotide sequence (I) encoding a CC Discosoma red fluorescent protein (DSRed) variant having a reduced CC propensity to oligomerise, comprising amino acid substitutions at the AB CC and/or AC interfaces of the wild-type DsRed sequence (SI) comprising 225 amino acids, given in the specification, where the substitutions result CC in reduced propensity of the DsRed variant to form tetramers. (I) is CC useful for detecting transcriptional activity by providing a host cells constining a vector which comprises (I) operatively linked to an CC expression control sequence, and assaying fluorescence of the variant fluorescent protein fluorescence, and assaying fluorescence of the variant fluorescent cells constining a fusion protein is useful for the analysis of in vivo considerable in protein is useful for the analysis of in vivo considerable in susful for the analysis of in vivo considerable in produced, where the target protein and amount of a carget protein produced, where the target protein and amount of a complement to or alternative for the green fluorescent protein or its spectral variant, for detecting induction of transcriptions, in capplications involving fluorescence energy resonance transfer (FRET), considerable and acceptors towards or away from each other, for making contains an enzyme or for detecting induction of transcriptions, in considerable for ions and molecules such as Ca2+, Zn2+, for identifying the protein for identifying a region or condition that regulates the activity of an expression control sequence. This sequence encodes Discosoma red constant dimerz.
            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting transcriptional activity.
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24-MAY-2001;
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                                                                                                                                      Sequence
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CAMPBELL R
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                                                                                                                                       681 BP; 145 A; 231 C;
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2001US-00866538.
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US-10-006-922A-12 (1-225) x ADC24130 (1-681)

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                                                                                                                   Discosoma
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                                   WO2003086446-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHis
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                                                                                                                                                                                                                                                                                               CTGTTCCTG 678
                                                                                                                                                                                                                                                                                                                     LeuPheLeu 225
                                                                                                                                                                                                                                                                                                                                             TCCCACAACGAGGACTACACCATCGTGGAACAGTACGAGCGCTCCGAGGGCCGCCACCAC
                                                                                                                                                                                                                                                                                                                                                         SerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArgHisHis
                                                                                                                                                                                                                                                                                                                                                                                           GCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACACCAAGCTGGACATCACC
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                                                                                                                                                                            red
                                                                                                                                                                                                  (first entry)
                                                                                                                                         fluorescent protein; DsRed; fluorescence; red wavelength; on; tetramerization; immunoassay; hybridization assay.
                                                                                                                                                                           fluorescent protein (DsRed) variant dimer2 coding sequence
                                                                                          Location/Qualifiers
                                                          'product= "DaRed variant dimer2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, usefi in molecular biology, e.g. in immunoassays or in tracking protein movement in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 681 BP; 145 A; 231 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding sequence for the variant dimer2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 7; 166pp; English.
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29-JUL-2002; 2002US-00209208.
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                                                                                    GlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysVal
                                                                                                                                                 LysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGly
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RESULT 72

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The present sequence is the nucleotide sequence of humanised dirF9583/dmrP952. Amplified wild-type coding region fragments from drFP583 and dmrP9592 were digested with restriction endonucleases and combined cogether to produce a hybrid construct. drFP583 is a full-length cDNA encoding a novel fluorescent protein (nFP) from Discosoma sp. "red", a non-bioluminescent species of the Class Anthozoa. The hybrid sequence was changed to optimise the codons for expression of the protein in mammalian cells. Fluorescent proteins can be used in fluorescent labeling, a useful tool for marking a protein, cell or organism of interest. Unlike other markers used in protein labeling, such as beta-galactosidase and luciferase, fluorescent proteins do not require an exogenous cofactor or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1998;
14-OCT-1999;
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fluorescent labeling; hybrid;
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                                                                                                                                                                                                                                                                                                                                                                              fluorescent protein from non-bioluminescent for fluorescent labeling and as markers.
                                                                                                                                                                                                                                                                                                                            6; Page 77; 86pp;
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                                     US-10-006-922A-12 (1-225) x AAD46280
                                                                                                                                                                                            The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is a DNA encoding Discosoma sp. drFP583/dmFP592 (6/9Q) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescence activated cell sorting application; fluorescent timer; biosensor; fluorescence resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; subsection; second messenger detector; drFP583 protein; dmFP592 protein
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                                                                                                                                                                                                                                                                                                                                                                         applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 incorporated by random mutagenesis. Fluorescent proteins can be used in fluorescent labeling, a useful tool for marking a protein; call or organism of interest. Unlike other markers used in protein labeling, such as beta-galactosidase and luciferase, fluorescent proteins do not require an exogenous cofactor or substrate. Methods involving fluorescent proteins are also less laborious and less difficult to control than the traditional methods of fluorescent labeling, where a protein of interest is purified and then covalently conjugated to a fluorophore derivative. Novel fluorescent proteins isolated from species of the Class Anthozoa can be used as markers for gene expression and protein localization studies, and in fluorescence resonance energy transfer (FRET) reactions. They may have improved properties and better suitability for larger excitations compared to prior art fluorescent proteins such as green
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The present sequence is derived from the nucleotide sequence of humanised hybrid drpps83/dnpps92. drpps83 is a full-length cDNA encoding a novel fluorescent protein (npp) from Discosoma sp. "red", a non-bioluminescent species of the Class Anthozoa. The hybrid sequence was changed to optimise the codons for expression of the protein in mammalian cells. The present sequence encodes three substitutions, K15Q, K83M and T217S, which were incorporated by random mutagenesis. Pluorescent proteins can be used in fluorescent labeling, a useful tool for marking a protein, cell or organism of interest. Unlike other markers used in protein do not require an exogenous cofactor or substrate. Methods involving fluorescent proteins are also less laborious and less difficult to control than the
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                                                                                                                                                                                                                                                                               LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                                                                                                                                                                                                                                                                                  AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly
                                                                                                                         TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrTyrValAspSerLysLeuAsp
                                                                                                                                                         IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                                                             CGGGGCTGGGAGGCCAGCAGCGAGCGGCTCTACCCCCGGGACGGCGTGCTCAAGGGCGAC
                                                                                                                                                                                                                                                                GAGGTGAAGTTCATCGGCGTGAACTTCCCCAGCGACGGCCCCGTGATGCAGCGGCGGACC
                                                                                                                                                                                                                                                                                                                    GACGGCGCGTGGTGACCGTGAGCCAGGACAGCCTCCAAGGACGGCTGCTTCATCTAC
                                                                                                                                                                                                                                                                                                                                                                       GACTACATGAAGCTCAGCTTCCCCCGAGGGCTTCAAGTGGGAGCGGGTGATGAACTTCGAG
                                                                                                                                                                                                                                                                                                                                                                                      AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                           CTCAGCCCCAGTTCCAGTACGGCAGCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGCAGCGTGAAGCTCATGGTGACCAAGGGCGGCCCCTTCCCCCTTCGCCTTCGACATC
                   HisHisLeuPheLeu
                                                    ATCACCAGCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGGTCCGAGGGCCGG
                                                                   TACATGGCCAAGAAGCCCGTGCAGCTCCCCGGCTACTACTACGTGGACAGCAAGCTCGAC
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RESULT 76 AAA28958 ID AAA28 XX

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standard; cDNA;

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DB:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                         US-10-006-922A-12 (1-225) x AAA28958 (1-876)
                                                                                                                                                                                                                                                                                            This cDNA encodes a fluorescent protein (dmFP592) from Discosoma sp. "magenta", a non-bioluminescent species of the genera Anthozoa. The fluorescent colour is observed under usual white light or ultraviolet light. It has an absorbance maximum at 573 nm and an emmission maximum at 593 nm. The polynucleotides of the invention can be used to produce the proteins recombinantly, and as a source of primers and probes for identifying related proteins. The fluorescent proteins have applications in fluorescent labeling, as fluorescent markers for gene expression and protein localization studies, and in fluorescence resonance energy transfer (FRET) reactions. They may have improved properties and better suitability for larger excitations, compared to prior art fluorescent proteins such as green fluorescent protein from Aequorea victoria, which has an excitation maximum at 395 nm, a second excitation peak at 475 nm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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P-PSDB; AAY92894.
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fluorescence resonance energy transfer reaction; FRET; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Discosoma sp.
                                                                                                                                                                                                                                                           Sequence 876 BP; 256 A; 165 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 54-55; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fluorescent protein from non-bioluminescent Discosoma species, useful for fluorescent labeling and as markers.
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19-NOV-1999;
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                                        ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                           MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly
                                                                            ATGAGTTGTTCCAAGAATGTGATCAAGGAGTTCATGAGGTTCAAGGTTCGTATGGAAGGA
HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                         ACGGTCAATGGGCACGAGTTTGAAATAAAAGGCGAAGGTGAAGGGAGGCCTTACGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "magenta" dmFP592 cDNA encoding a fluorescent protein
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99US-00444341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "fluorescent_protein"
                                                                                                                                                         2.75e-124
1085.50
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89.42%
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09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     magenta.
99US-00418529.
99US-00418917.
99US-00418922.
99US-00444338.
99US-00444331.
99US-00457556.
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/product= "Chromo/fluorescent protein, dmFP592 (NFP-9)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a Discosoma sp. magenta chromo/fluorescent protein, dmpP592 (NPP-9) cDNA. NPP-9 is present in an environment other than its natural environment and has an absorbance maximum ranging from 375nm to 775nm and more usually from 560nm to 590nm and emission maximum ranging from 395nm to 795nm and more usually from 580 to 610nm. The chromoproteins or fluorescent proteins are useful as labels in analyte detection assays, as selectable markers in recombinant DNA applications, as biosensors in prokaryotic and ewkaryotic cells e.g. as pH indicator and as in vivo markers in animals. They are also useful in sunscreens and as selective filters. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An Anthozoa chromo- or fluorescent protein (P1) present in an envother than its natural environment, useful as a label in analyte detection assays and as a selectable marker in recombinant DNA applications.
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AspG1yG1yVa1Va1ThrVa1ThrG1nAspSerSerLeuG1nAspG1yCysPheI1eTyr
                                                            TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAACACCCTGCCGACATACCA
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                                                                                                                                                                                                                                               Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosome-based platform; artificial chromosome; eukaryotic chroatt site; integrase; recombinase; ACes; gene therapy; transgenic platform artificial chromosome expression system; gene; ds.
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DB; ABP96651.
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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (ACss) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for

Example 1; Page 191-192; 272pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcall fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention
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 ArgHisHisLeuPheLeu 225
                                                                AspIleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGly
                                                                                                                                           TyrMetAlaLysLysPro---ValGlnLeuProGlyTyrTyrTyrTyrValAspSerLysLeu
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The invention describes a polynucleotide sequence (I) encoding a CC Discosoma red fluorescent protein (DBRed) variant having a reduced CC propensity to oligomerise, comprising amino acid substitutions at the AB CC and/or AC interfaces of the wild-type DBRed sequence (SI) comprising 225 and/or AC interfaces of the wild-type DBRed sequence (SI) comprising 225 CC amino acids, given in the specification, where the substitutions result in reduced propensity of the DBRed variant to form tetramers. (I) is CC useful for detecting transcriptional activity by providing a host cells CC conatining a vector which comprises (I) operatively linked to an CC expression control sequence, and an unit to assay the variant fluorescent protein fluorescence, and assaying fluorescence of the variant CC fluorescence is indicative of transcriptional activity. A polynucleotide cencoding a fusion protein is useful for the analysis of in vivo CC localisation or trafficking of a polypeptide of interest. A polypeptide CC marker is useful as markers to identify the location and amount of a CC target protein produced, where the target protein and amount of a CC target protein variant, for detecting induction of transcriptions, in CC applications involving fluorescence energy resonance transfer (PRET), which detects events as the function of the movement of fluorescent contains an enzyme or away from each other, for making CC fluorescent sensors for protein kinase and phosphatase activities or indicators for ions and molecules such as Ca2+, Zn2+, for identifying the contains an enzyme or for determining the plot the sample. (I) is smalle contains an enzyme or for determining the plot the sample. (I) is
                                                          sample contains an enzyme or for determining the pH of the sample. (I) is useful for identifying a region or condition that regulates the activity of an expression control sequence. This sequence encodes Discosoma red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Discosoma red fluorescent protein; DsRed; AB interface; AC in fluorescent protein variant; transcription induction detection fluorescence energy resonance transfer; FRET; protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting
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24-MAY-2001; 2001US-00866538.
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                                          fluorescent protein variant mRFP1.
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CAMPBELL R E.
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                          red fluorescent protein; DsRed; fluorescence; red wavelength; oligomerization; tetramerization; immunoassay; hybridization assay; gene;
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                                                                                                                                                                                                                                                                                                         TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAAGACCGACATCAAGCTGGAC
                                                                                                                                                                                                                                                                                                                                                             <u>ATCAAGATGAGGCTGAAGGACGGCGGCCACTACGACGCCGAGGTCAAGACCACC</u>
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                                                                                             (first entry)
                                                                fluorescent protein (DsRed) variant mRFP1 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, usefi in molecular biology, e.g. in immunoassays or in tracking protein
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29-JUL-2002; 2002US-00209208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 9; 166pp; English
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AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
                                       CTGTCCCCTCAGTTCCAGTACGGCTCCAAGGCCTACGTGAAGCACCCCGGCCGACATCCCC
                                                          LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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/product= "DsRed variant mRFP1 protein"
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                                                                              Novel fluorescent protein existing as monomer and isolated from Fungia and Montipora species, useful for labeling and analyzing location and movement of intracellular organelles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fluorescence;
mitochondria;
                                        Example 10; SEQ ID NO 50; 218pp; Japanese
                                                                                                                                                                WPI; 2005-444979/45.
P-PSDB; AEA54910.
                                                                                                                                                                                                                                          Miyawaki A,
                                                                                                                                                                                                                                                                                                                                               03-DEC-2003; 2003JP-00404472.
27-JAN-2004; 2004JP-00018344.
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MEDICAL & BIOLOGICAL LAB CO LTD.
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ds; gene; enhanced green fluorescent protein; EGFP;
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invention relates to a novel fluorescent protein existing

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Alignment Scores: Pred. No.:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monomer and comprising any one of SEQ ID No. 1-29 (odd SEQ ID numbers) given in the specification, or any one of the sequences chosen from SEQ ID No. 1-29 (odd SEQ ID numbers), with one or more amino acid substitutions, deletions and/or additions, and having fluorescent characteristics. The fusion protein of the invention may be useful for analyzing the location or movement of a protein in cell in vivo and for labeling and analyzing the location or movement of intracellular organelles, such as mitochondria. The current sequence is that of the fluorescence-related enhanced green fluorescent protein (EGFP)-caspase-3 DEVD linker-mRFP(x2) fusion DNA of the invention.
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                                                                                               IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                                                      TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCCTACAAGACCGACATCAAGCTGGAC
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CC fragments of a protein or mutant protein, where the fragments generate an optically detectable signal when associated, and each of the mutant CC protein fragments is fused to a separate molecule. Also described are: CC protein fragment sis fused to a separate molecule. Also described are: CC protein fragment complementation assays (PCAs) for detection of molecular interactions, involving reassembling separate fragments from an optically CC detectable protein, and detecting the reassembly by units of reconstitution of activity of the optically detectable protein, where the creassembly of the fragments is operated by the interaction of molecular CC domains fused to each fragment, and is independent of other molecular CC grocesses; detecting biomolecular interaction, involving selecting an CC optically detectable protein such that the fragmentation results in CC reversible loss of protein such that the fragmentation results in CC reversible loss of protein such that the fragmentation results of the optically detectable protein separately to other molecules, reassociating the protein fragments, and detecting the resulting optical CC signal, designing and engineering of PCAs based on fluorescent protein; and a method and composition for the construction of multi-color PCAs. CC (1) is useful in PCAs and other assays for drug discovery, target walldation, high-throughput screening, high-content screening, pathway of mapping, drug mechanism-of-action studies, biosensors and diagnostics. (1) is useful for engineering different colour PCAs for a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2000; 2000US-00499464.

04-MAY-2002; 2002US-00154758.

29-JAN-2003; 2003US-00353090.

09-APR-2003; 2003US-0461133P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition useful in protein fragment complementation assays for drug discovery and high-throughput screening, comprising complementary fragments of protein or mutant protein, generating optically detectable
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MACDONALD M L.
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                                           ADL46282;
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                                                                                                                                                                                                                                           ATCAAGATGAGGCTGAAGGTGAAGGACGGCGGCCACTACGACGCCGAGGTCAAGACCACC
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                                                                                                                                                     ATCACCTCCCACAACGAGGACTACACCATCGTGGAACAGTACGAGCGCGCCGAGGGCCGC
                                                                                                                                                                                                             TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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Discosoma red fluorescent protein (DsRed) variant mRFP1.1 coding sequence.

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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DRRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(8) of the wild-type DSRed sequence, where the substitutions result in reduced propensity of the DBRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DSRed variant mRFP1.1 coding sequence. The protein contains a Q66M and a T147S mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful molecular biology, e.g. in immunoassays or in tracking protein movement in cells.
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oligomerization; tetramerization; immunoassay; hybridization assay; gene;
ds.
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29-JUL-2002; 2002US-00209208.
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                                                                                                                        1 MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly 20
                                                                                               TCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCCGCCCCTACGAGGGC
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Matches:
Conservative:
Mismatches:
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661	221	601	201	541	181	481	161	421	141	361	121	301	101	241	81	181	61
. CAC 663	. HiB 221	ATCACCTCCCACAACGAGGACTACACCATCGTGGAACAGTACGAGCGCCGAGGGCCGC 660	IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg 220	. TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAAGACCGACATCAAGCTGGAC 600	TyrMetAlaLysLysProValGlnLeuProGlYTyrTyrTyrValAspSerLysLeuAsp 200	ATCAAGATGAGGCTGAAGCTGAAGGACGGCGGCGACTACGACGCCGAGGTCAAGACCACC 540	IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180	. ATGGGCTGGGAGGCCTCCTCCGAGCGGATGTACCCCGAGGACGGCCCCTGAAGGGCGAG 480	MetGlyTrpGluAlaSer	AAGGTGAAGCTGCGCGCACCAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGAAGACC 420	. LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140	GACGGCGGGGTGGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTAC 360	AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120	GACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG 300	AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100	CTGTCCCCTCAGTTCATGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCC 240	LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80

Search completed: January 12, 2006, 12:55:37 Job time : 528 secs

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Result
No.
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-MODEL-frame+ p2n.model -DEV-xlp
-MODEL-frame+ p2n.model -DEV-xlp
-Q-/cgn2 1/USPTO spool p/US10006922/runat 10012006 162504 19128/app_query.fasta_1.391
-Q-/cgn2 1/USPTO spool p/US10006922/runat 10012006 162504 19128/app_query.fasta_1.391
-DB-EST -QFWT=fastap -SUFFIX-p2nminscr.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=69 -ALIGN=500 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -THR_NINEN=0 -MAXIEN=200000000
-USER-US10006922 -GCGN 1 1 8010 @runat 10012006 162504 19128 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 69%
Maximum Match 100%
Listing first 500 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters ---
Search completed: January 12, 2006, 14:59:07 Job time : 3747 Becs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                           No matches found
                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                      Score
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1214
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Match Length DB
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss1:*
gb_gss2:*
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gb_est6:*
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GenCore version Copyright (c) 1993 - 2006

5.1.6 Compugen Ltd.

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Command line parameters:

-MODEL-frame+_D2n.model -DEV=xlp
-MODEL-frame+_D2n.model -DEV=xlp
-Q=/Ggn2_1/USPTO_6pool_p/US10066922/runat_10012006_162505_19142/app_query.fasta_1.391
-Q=/Ggn2_1/USPTO_6pool_p/US1006922/runat_10012006_162505_19142/app_query.fasta_1.391
-DB=Issued_Patents_NA -QFMT=fastap_-SUPFIX=p2nminser.rrni -MINMATCH=0.1
-LOOPEXY=0 -UNITS=b1ts -STAKT=1 -END=-1 -MATRIX=b10sum62
-TRANS=human40.cd4 -L1sTs=500 -DOCALIGN=200 -THR END=-1 -THR MAX=100
-THR_MIN=69 -ALIGN=500 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-THR_MIN=69 -ALIGN=500 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000
                                                                                                                                                   Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 500 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -USER=US10006922 @CGN 1 1 290 @runat 10012006 162505 19142 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Match
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     100.0
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100.0
99.7
99.7
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US-09-459-956-6
US-09-866-538-11
US-09-865-291-11
US-10-152-296-1
US-10-001-189-45
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  Sequence 6, Appli
Sequence 11, Appl
Sequence 11, Appli
Sequence 1, Appli
Sequence 45, Appl
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ALIGNMENTS

140

360 120 300

160 420

480

540

100 240 80 180 60 120

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tsien, Roger Y.

APPLICANT: Gonzalez, III, Jesus E.

APPLICANT: Gonzalez, III, Jesus E.

APPLICANT: Gonzalez, III, Jesus E.

TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POT

TITLE OF INVENTION: OPTICAL METHODS

FILE REFERENCE: REGEN1290-4

CURRENT APPLICATION NUMBER: U8/09/459,956

CURRENT FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 08/765,860

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR APPLICATION NUMBER: PCT/US96/09652

PRIOR APPLICATION NUMBER: PCT/US96/09652

PRIOR FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-006-922A-12 (1-225) x US-09-459-956-6 (1-678)
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SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 678
TYPE: DNA
ORGANISM: Discosoma
 481
                               161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                   HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAGGTCTTCCAAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGCATGGAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGGTCAATGGGCACGAGTTTGAAATAGAAGGCGAAGGAGAGGGGAGAGGCCATACGAAGGC
                                                                                                                                                                                                                                                                                                                  TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCA
                                                                                                                                                                                                                                                                                                                                        LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                                                                                                                                                                                                                                                                                                   CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGGACCTTTGCCATTTGCTTGGGATATT
                                                                               LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                                                                                                        GACGGTGGCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTAC
                                                                                                                                                                                                            AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                   AAGGTCAAGTTCATTGGCGTGAACTTTCCTTCCGATGGACCTGTTATGCAAAAGAAGACA
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Indels:
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653

160 533 180 593 200

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; TYPE: DNA; ORGANISM: Discosoma sp; FEATURE: ; NAME/KEY: CDS; LOCATION: (54)..(731) US-09-866-538-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGET
APPLICANT: Campbell, Robert
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROFILE REFERENCE: REGEN1530-2
FILE REFERENCE: REGEN1530-2
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VETSION 3.0
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Query Match:
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US-09-866-538-11
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                                                                                  AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr
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Best Local Similarity:
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APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
FILE REFERENCE: REGEN1550
CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 859
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LOCATION: (54)..(731)
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            AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                  ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
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REQUENCE 1, Application US/10152296

REQUENCE 1, Application US/10152296

Patent No. 672537

REMERAL INFORMATION:

APPLICANT: Peealle, Beau

APPLICANT: Rigel Pharmaceuticals, Incorporated

APPLICANT: Rigel Pharmaceuticals, Incorporated

APPLICANT: Rigel Pharmaceuticals, Incorporated

FILE REFERENCE: 021044-000110US

FILE REFERENCE: 021044-000110US

CURRENT APPLICATION NUMBER: US/10/152,296

CURRENT FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: US 60/291,871

PRIOR APPLICATION NUMBER: US 60/291,871

PRIOR FILING DATE: 2001-05-18

NUMBER OF SEQ ID NOS: 2

SOPTMARE: PatentIn Ver. 2.1

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                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:mammalian OTHER INFORMATION: codon-optimized variant (DsRED) of Discosoma OTHER INFORMATION: "red" red fluorescent protein (RFP) FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(723)
OTHER INFORMATION: DBRED
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ORGANISM: Artificial Sequence
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 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
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LENGTH: 6984

TORANISM: Artificial Sequence
CARTURE:
OTHER INFORMATION: Description
OTHER INFORMATION: pBXP3-DsRed-
US-10-001-189-45
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US-10-001-189-45
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                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION TITLE OF INVENTION: VECTOR PIGGYBAC FILE REFERENCE: 835910-92098

CURRENT APPLICATION NUMBER: US/10/001,189

CURRENT FILING DATE: 2001-10-30

PRIOR APPLICATION NUMBER: 60/244,984

PRIOR APPLICATION NUMBER: 60/244,677

PRIOR APPLICATION NUMBER: 60/244,677

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PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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-Q-/cgn2 1/USFTO spool p/US10006922/runat 10012006 162505 19171/app_query.fasta_1.391
-DB=PublIshed Applications NA Main -OFMT=fastap -SUFFIX=p2mminscr:rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=500 -DCCALIGN=200 -THR SCORE=pct
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=500 -DCCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=69 -ALIGN=500 -MODEL-LOCAL -OUTFMT=pto -NORM-ext
-HAPBSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 11, Appli
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Result No.

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FILE REFERENCE: REGEN1290-5
CURRENT APPLICATION NUMBER: US/09/967,772
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/459,956
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-12-19
PRIOR PRIOR PRIOR NUMBER: PCT/ US96/09652
PRIOR TILING DATE: 1996-06-06
PRIOR TILING DATE: 1996-06-06
PRIOR APPLICATION NUMBER: US 08/481,977
PRIOR APPLICATION NUMBER: US 08/481,977
PRIOR PILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 22
SOPTWARE: PATENTIN VETSION 3.0
SEQ ID NO 6
SEQ ID NO 6
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US-09-967-772-6

(Sequence 6, Application US/09967772

; Patent No. US20020164577A1

; GENERAL INFORMATION:
    APPLICANT: THE RESENTS OF THE UNIVERSITY OF CALIFORNIA
    APPLICANT: GONZALEZ, Jesus
    APPLICANT: GONZALEZ, Jesus
    APPLICANT: OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL |
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Query Match:
DB:
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; TYPE: DNA
; ORGANISM: Discosoma
US-09-967-772-6
                                                                                                                                                                                                                                                                                              US-10-006-922A-12 (1-225) x US-09-967-772-6 (1-678)
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                                           LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
                                                                                                       HisAsnThrVallysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle
                                                                                                                                                                               ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
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US-10-931-304-101
US-10-931-304-90
US-10-931-304-93
US-10-931-304-95
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Conservative:
Mismatches:
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Gaps:
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                                                                  Alignment & Pred. No.:
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                Percent Similarity:
Best Local Similarity:
                                                    Score:
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                                                                                                                                                                                          SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lukyanov, Sergey A
APPLICANT: Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terskikh, Alexey
                                                                                                                                                                                                            SOFTWARE: FastSEQ
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                     TYPE: DNA ORGANISM: Discosoma
                                                                                                                                                                           LENGTH: 678
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              Length:
Matches:
Conservative:
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Sequence 7, Application US/10081864

Publication No. US20030022287A1

GENERAL INFORMATION:

APPLICANT: Lukyanov, Sergey

APPLICANT: Lukyanov, Konstantin

APPLICANT: Lukyanov, Konstantin

APPLICANT: Fradkov, Alexandr

APPLICANT: Fradkov, Arcady

APPLICANT: Fradkov, Arcady

TITLE OF INVENTION: Methods for Using the Same

FILE REFERENCE: CLON-067

CURRENT APPLICATION NUMBER: US/10/081,864

CURRENT APPLICATION NUMBER: 10/006,922

PRIOR APPLICATION NUMBER: 10/006,922

PRIOR APPLICATION NUMBER: 60/270,983

PRIOR FILING DATE: 2001-02-21

NUMBER OF SEQ ID NOS: 30

SOFTMARE: FastSEQ for Windows Version 4.0
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        Sequence 2, Application US/10121258

Publication No. US20030059835A1

GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR
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TYPE: DNA
ORGANISM: Discosoma
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REFERENCE: UC083.1CP2CP1

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CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOPTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 678
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; LOCATION: (1)...(678)
; OTHER INFORMATION: wild-type DsRed
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ORGANISM: Discosoma
FEATURE:
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                IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                         TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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Sequence 1, Application US/10315920

Sequence 1, Application WS/10315920

Publication No. US20030175809A1

GENERAL INFORMATION:
APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Terskikh, Alexey

TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND
ITILE OF INVENTION: FOR THEIR USE

FILE REFERENCE: CLON-077CIP

CURRENT APPLICATION NUMBER: US/10/315,920

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: 60/211,607

PRIOR FILING DATE: 2000-06-14

PRIOR PILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 22

SOPTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 678
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Sequence 3, Application US/10132067

Publication No. US20030203355A1

GENERAL INFORMATION:
APPLICANT: Bradbury, Andrew
APPLICANT: Zeytun, Ahmet
APPLICANT: Waldo, Geoffrey
APPLICANT: Waldo, Geoffrey
TITLE OF INVENTION: Fluorobodies: Binding Ligands With Int:
TITLE OF INVENTION: Pluorescence
FILE REPERENCE: 02162-000600US

CURRENT APPLICATION NUMBER: US/10/132,067

CURRENT FILING DATE: 2002-04-24

NUMBER OF SEQ ID NOS: 48

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 3
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ORGANISM: Discosoma sp.
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                                                                   LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspTlePro
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Query Match:
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; TYPE: DNA
; ORGANISM: Discosoma
US-10-335-517-6
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/967,772
PRIOR FILING DATE: 2001-09-28
PRIOR PPLICATION NUMBER: US 09/459,956
PRIOR PILING DATE: 1999-12-13
PRIOR PILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR PILING DATE: 1996-12-19
PRIOR PILING DATE: 1996-12-19
PRIOR PILING DATE: 1996-06-06
PRIOR PILING DATE: 1996-06-06
PRIOR PILING DATE: 1996-06-07
PRIOR PILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 22
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US-10-335-517-6
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Publication No. US20030207248A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: THE REGERTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: TSIEN, ROGER APPLICANT: GONZALEZ, Jesus TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIF FILE REFERENCE: REGER1290-5 CURRENT APPLICATION NUMBER: US/10/335,517 CURRENT FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
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ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
                                                 MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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Sequence 6, Application US/10334288

Publication No. US20040002123A1

GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: GONZALEZ, JESUS
FILE REFERENCE: REGEN1290-5

CURRENT APPLICATION NUMBER: US/10/334,288

CURRENT APPLICATION NUMBER: US/09/967,772

PRIOR APPLICATION NUMBER: US/09/967,772

PRIOR APPLICATION NUMBER: US/09/967,772

PRIOR APPLICATION NUMBER: US/09/966

PRIOR APPLICATION NUMBER: US 09/459,956

PRIOR APPLICATION NUMBER: US 08/765,860

PRIOR FILING DATE: 1996-12-13

PRIOR APPLICATION NUMBER: US 08/765,860

PRIOR FILING DATE: 1996-12-19

PRIOR FILING DATE: 1996-06-06

PRIOR APPLICATION NUMBER: US 08/765,860

PRIOR FILING DATE: 1996-06-07

PRIOR APPLICATION NUMBER: US 08/765,860

PRIOR FILING DATE: 1996-06-07

PRIOR FILING DATE: 1996-06-07

PRIOR APPLICATION NUMBER: US 08/481,977

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1996-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1996-06-07

PRIOR FILING DATE: 1996-06-07

PRIOR PRIO
               ; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma
US-10-334-288-6
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Query Match:
DB:
APPLICANT: Nelson, David
APPLICANT: Zamiara, Elize
APPLICANT: Tsien, ROger
APPLICANT: Tsien, ROger
APPLICANT: Tsien, ROger
FITTLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS
FILE REFERENCE: 15916-032US1
CURRENT APPLICATION NUMBER: US/10/311,030
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/US01/04625
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/184,732
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, NUMBER OF SEQ ID NOS: 12
, SOFTWARE: FASTSEQ for Windows Version 4.0
, SEQ ID NO 5
, SEQ ID NO 5
, LENGTH: 678
, TYPE: DNA
, ORGANISM: Discosoma sp.
US-10-311-030-5
RESULT 10
US-10-656-029-21
US-10-656-029-21
; Bequence 21, Application US/10656029
; Publication No. US20050003367A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INC
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ORGANISM: Discosoma s
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(678)
OTHER INFORMATION: fl
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FILE REFERENCE: VPI/02-143WO2
CURRENT APPLICATION NUMBER: US/10/656,029
CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: 60/408,297
PRIOR APPLICATION NUMBER: 60/408,297
PRIOR PILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 86
SOPTWARE: Patentin version 3.2
SEQ ID NO 21
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              | IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
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                                                               TyrMetAlaLysLysBroValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAAGAACCGAGGGACGC
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Sequence 27, Application US/10505486
Publication No. US20050118639A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: P03-0006PCT
CURRENT APPLICATION NUMBER: US/10/505,486
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: JP 2002-45728
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: JP 2002-213949
PRIOR APPLICATION NUMBER: JP 2002-233
PRIOR APPLICATION NUMBER: JP 2002-298237
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 233
SEQ ID NO 27
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Best Local Similarity:
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; TYPE: DNA
; ORGANISM: Discosoma
US-10-505-486-27
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US-10-505-486-27
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                     IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
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US-10-844-064A-1
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APPLICANT: Bevis, Brooke
APPLICANT: Glick, Benjamin
TITLE OF INVENTION: RAPIDLY MATURING FLUORESCENT PROTEINS AND METHODS FOR USING THE
FILE REFERENCE: 092234-9006
CURRENT APPLICATION NUMBER: US/10/844,064A
CURRENT FILING DATE: 2004-05-11
PRIOR APPLICATION NUMBER: PCT/US02/40539
PRIOR APPLICATION NUMBER: US 60/341,723
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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ORGANISM: Discosoma
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                                                                      AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAK.
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOPTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 678
TYPE: DNA
CREANISM: Discosoma 8D.
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, NAME/KEY: misc_feature
, LOCATION: (1)...(678)
, OTHER INFORMATION: wild-
US-10-931-304-2
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Best Local Similarity:
Query Match:
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US-10-931-304-2
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H18A8nThrValLy8LeuLy8ValThrLy8GlyGlyProLeuProPheAlaTrpAspIle
                                                                 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                                                           MetArgSerSerLysAsnVallleLysGluPheMetArgPheLysValArgMetGluGly
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N: wild-type DsRed
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                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                               FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SOPTWARE: PATENTIN VERSION 3.0
SEQ ID NO 66
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; NAME/KEY: CDS
; LOCATION: (54)..(731)
US-09-999-745-66
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                   US-10-006-922A-12 (1-225) x US-09-999-745-66
                                                                                                                                           Alignment Scores:
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Patent No. US20020157120A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
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TYPE: DNA
ORGANISM: Discosoma sp
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; TYPE: DNA; ORGANISM: Discosoma sp; FEATURE: NAME/KEY: CDS; LOCATION: (54)..(731) US-09-866-538-11
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; Sequence 11, Application US/09866538
; Publication No. US20030032088A1
; GENERAL INFORMATION:
Alignment Scores:
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                                                                                                                             APPLICANT: REGERTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: TSIEN, ROGET APPLICANT: TSIEN, ROGET TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS FILE REFERENCE: REGEN1530-2 CURRENT APPLICATION NUMBER: US/09/866,538 CURRENT FILING DATE: 2001-05-24 NUMBER OF SEQ ID NOS: 29 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO 11 LENGTH: 859
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                                      Sequence 11, Application US/09794308

Publication No. US20030170911A1

GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, Roger
APPLICANT: TSIEN, Roger
APPLICANT: TACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROFILE REFERENCE: REGEN1530
CURRENT APPLICATION UNMBER: US/09/794,308
CURRENT PILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 25
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US-09-794-308-11
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; TYPE: DNA
; ORGANISM: D18
; PEATURE:
; NAME/KEY: CDS
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Sequence 11, Application US/09865291
Publication No. US20030186229A1
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF
APPLICANT: TSIEN, Roger
APPLICANT: TING, Alice
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; APPLICANT: ZHANG, Jin
; TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF
; FILE REFERENCE: REGEN1550
; CURRENT APPLICATION NUMBER: US/09/865,291
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(731)
US-09-865-291-11
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CACCATCTGTTCCTT

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Sequence 12, Application US/10433640

Publication No. US20040115792A1

GENERAL INFORMATION:

APPLICANT: Lichtenberg-Frate, Hella
TITLE OF INVENTION: YEAST STRAIN FOR TESTING THE GENOTOXICITY AND CYTOTOXICITY OF

TITLE OF INVENTION: COMPLEX ENVIRONMENTAL CONTAMINATIONS

FILE REFERENCE: 1487/3

CURRENT APPLICATION NUMBER: US/10/433,640

CURRENT FILING DATE: 2003-10-02

FRIOR APPLICATION NUMBER: PCT/EPO1/14610

FRIOR APPLICATION NUMBER: DC 10061872.3

FRIOR APPLICATION NUMBER: DE 10061872.3

FRIOR FILING DATE: 2001-12-12

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patcentin version 3.2

SEQ ID NO 12

LENGTH: 859
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IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                         MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
                                                                                                                      LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                                                                                                                  GACGGTGGCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTAC
                                                                                                                                                                                   AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOPTWARE: Patentin version 3.0
SEQ ID NO 11
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APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENI530-2
CURRENT PEPLICATION NUMBER: US/10/885,988
CURRENT FILING DATE: 2004-07-06
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LOCATION: (54)..(731)
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                                                   GACGGTGGCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTAC
                                                                                                                     GACTATAAAAAGCTGTCATTTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACTTTGAA
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APPLICANT: VIOLIN, Jonathan
APPLICANT: NEWTON, Alexandra
APPLICANT: TSIEN, Roger
APPLICANT: TSIEN, Roger
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: Emission Ratiometric Indicators of Phosphorylation By C-Kinase
FILE REFERENCE: 39754-0891 CCPC1CP2
CURRENT APPLICATION NUMBER: US/10/857,622
CURRENT APPLICATION NUMBER: US 09/865,291
PRIOR APPLICATION NUMBER: US 09/865,291
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR APPLICATION NUMBER: US 09/792,553
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR PILING DATE: 1997-01-31
PRIOR PILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PastSEQ for Windows Version 4.0
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PEATURE:
NAME/KEY: CDS
LCCATION: (54)..(731)
US-10-857-622-11
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Best Local Similarity:
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Publication No. US20050026234A1
GENERAL INFORMATION:
APPLICANT: RECENTS OF THE UNIVERSITY
APPLICANT: VIOLIN, Jonathan
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                                    US-10-006-922A-12 (1-225) x US-09-797-496B-3 (1-3311)
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Publication No. US20030049597A1
GENERAL INFORMATION:
APPLICANT: Simon, Sanford M.
APPLICANT: Chen, Yu
APPLICANT: Chen, Yu
TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
FILE REFERENCE: 600-1-267
CURRENT APPLICATION NUMBER: US/09/797,496B
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial sequence
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Sequence 35, Application US/10006922

| Publication No. US20020197676A1
| GENERAL INFORMATION:
| APPLICANT: Labas, Yuli A. |
| APPLICANT: Fradkov, Arcady F. |
| APPLICANT: Labas, Yuli A. |
| APPLICANT: Matz, Mikhail V. |
| APPLICANT: Tarskikh, Alexey |
| TITLE OF INVENTION: No. US20020197676A1el Chromophores and TITLE OF INVENTION: Methods for Using the Same |
| FILE REFERENCE: CLON-035CIP |
| CURRENT APPLICATION NUMBER: US/10/006,922 |
| CURRENT FILING DATE: 1998-12-19 |
| PRIOR APPLICATION NUMBER: 09/120,330 |
| PRIOR APPLICATION NUMBER: 09/457,898 |
| PRIOR APPLICATION NUMBER: 09/457,898 |
| PRIOR APPLICATION NUMBER: 09/457,898 |
| PRIOR APPLICATION NUMBER: 09/458,447 |
| PRIOR APPLICATION NUMBER: 09/458,477 |
| PRIOR APP
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     RESULT 23
US-10-121-258-3
; Sequence 3, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: TBien, Roger
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LENGTH: 681
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotide s
OTHER INFORMATION: codon usage
US-10-121-258-3
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CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SEQ ID NO 3
SEQ ID NO 3
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Best Local Similarity:
Query Match:
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IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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                                                             TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
                                                                                                ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
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1210.00
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Matches:
Conservative:
Mismatches:
Indels:
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METHODS FOR MAKING SAME
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APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLI
TITLE OF INVENTION: PROTEIN VARIANTS AND ME'
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 23
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Best Local Similarity:
Query Match:
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OTHER INFORMATION:
US-10-121-258-23
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TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Zamiara, Elize
APPLICANT: Tsien, Roger
ITTLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS
FILE REFERENCE: 15916-032US1
CURRENT APPLICATION NUMBER: US/10/311,030
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/US01/04625
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/184,732
PRIOR APPLICATION NUMBER: US 60/184,732
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
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Publication No. US20040171107A1
GENERAL INFORMATION:
APPLICANT: Nelson, David
APPLICANT: Zamiara, Elize
APPLICANT: Tsien, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 681
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
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                                   LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80
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1210.00
100.00%
99.56%
99.67%
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Matches:
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APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAX
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT TILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FASESEQ for Windows Version 4.0
                                            Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-006-922A-12 (1-225) x US-10-931-304-3 (1-681)
                                                                                                                               Alignment Scores:
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US-10-931-304-3
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                                                                                                                 Pred. No.:
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                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: nucleotide sequence encoding OTHER INFORMATION: codon usage
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TYPE: DNA
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Conservative:
Mismatches:
Indels:
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APPLICANT: Campbell, Robert
APPLICANT: Gampbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAX
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT PILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/944,308
PRIOR APPLICATION NUMBER: 09/944,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-26
NUMBER OF SEQ ID NOS: 110
SEQ ID NO 23
                                                                                                                                                                                                     RESULT 27
US-10-931-304-23
J Sequence 23, Application US/10931304
Publication No. US20050196768A1
J GENERAL INFORMATION:
J GENERAL INFORMATION:
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             RESULT 28
US-10-311-030-11
US-10-311-030-11
; Sequence 11, Application US/10311030
; Publication No. US20040171107A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, David
; APPLICANT: Zamiara, Elize
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; CRANTURE:
; OTHER INFORMATION: nucleotide s
; OTHER INFORMATION: codon usage
US-10-931-304-23
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           HisHisLeuPheLeu
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                                                                                      TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
CACCACCTGTTCCTG
                                                                                                                                    ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
                                           ATCACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGC
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codon usage
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APPLICANT: Tsien, Roger
TITLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS
FILE REFERENCE: 15916-032US1
CURRENT APPLICATION UNUMBER: US/10/311,030
CURRENT FILING DATE: 2002-12-10
FRIOR APPLICATION NUMBER: PCT/US01/04625
FRIOR APPLICATION NUMBER: PCT/US01/04625
FRIOR APPLICATION NUMBER: US 60/184,732
FRIOR APPLICATION NUMBER: US 60/184,732
FRIOR APPLICATION NUMBER: US 60/184,732
FRIOR FILING DATE: 2000-02-23
SUMMBER OF 850 ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 713
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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (19)...(696)
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IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                           TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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                                                                                   ATCCACAAGGCCCTGAAGCTGAAGGACGGCCGCCACTACCTGGTGGAGTTCAAGTCCATC
                                                                                                    IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                         MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                AAGGTGAAGTTCATCGGCGTGAACTTCCCCAGCGACGGCCCCCGTGATGCAGAAGAAGACCC
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Best Local Similarity:
Query Match:
DB:
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US-10-311-030-12/c
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Publication No. US20040171107A1
GENERAL INFORMATION:
APPLICANT: Nelson, David
APPLICANT: Zamiara, Elize
APPLICANT: Tsien, Roger
TITLE OF INVENTION: MODIFIED FLUORESCENT PROTEINS
FILE REFERENCE: 15916-032US1
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SEQ ID NO 12
LENGTH: 713
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CURRENT FILLING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/US01/04625
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/184,732
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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                                                                                  LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                                                                                        GACGGCGGCGTGGTGACCGTGACCCAGGACAGCAGCCTGCAGGACGGCTGCTTCATCTAC
                                                                                                                                                                                                                                             AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
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                                                              AAGGTGAAGTTCATCGGCGTGAACTTCCCCCAGCGACGGCCCCGTGATGCAGAAGAAGACC
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Matches:
Conservative:
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Gaps:
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663 220 603 200 543 160

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Sequence 1, Application US/10152296

| Publication No. US20030077730A1
| GENERAL INFORMATION:
| APPLICANT: Peelle, Beau
| APPLICANT: Night Pharmaceuticals, Incorporated
| TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells
| TITLE OF INVENTION: UNMBER: US/10/152,296
| CURRENT APPLICATION NUMBER: US/10/152,296
| CURRENT APPLICATION NUMBER: US 60/291,871
| PRIOR APPLICATION NUMBER: US 60/291,871
| PRIOR PILING DATE: 2001-05-18
| NUMBER OF SEQ ID NOS: 2
| SOPTWARE: Patentin Ver. 2.1
| SEQ ID NO: 1
| LENGTH: 723
| TYPE: DNA
| ORGANISM: Artificial Sequence
| PEATURE: OTHER INFORMATION: Description of Artificial Sequence:mammalian OTHER INFORMATION: Codon-optimized variant (DBRED) of Discosoma sp. OTHER INFORMATION: "red" red fluorescent protein (RFP)
| PEATURE: OTHER INFORMATION: "red" red fluorescent protein (RFP)
                                                                                                                                                                                                                                                                                                              Percent Similarity:
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OTHER INFORMATION: DSRED
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                                                                                       H18A8nThrValLy8LeuLy8ValThrLy8GlyGlyProLeuProPheAlaTrpAspIle
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                       LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Directed Evolution of Protein:
FILE REFERENCE: 02044-000110US
CURRENT APPLICATION NUMBER: US/10/739,656
CURRENT FILING DATE: 2003-12-17
PRIOR APPLICATION NUMBER: US/10/152,296
PRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/291,871
PRIOR APPLICATION NUMBER: US 60/291,871
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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US-10-739-656-1
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   US-10-006-922A-12 (1-225) x US-10-739-656-1 (1-723)
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                                                                                                                                                                                                                                                                                                                 LENGTH: 723
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:mammalian OTHER INFORMATION: codon-optimized variant (DsRED) of Discosoma OTHER INFORMATION: "red" red fluorescent protein (RFP) FEATURE:
                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (1)..(723)
OTHER INFORMATION: DSRED
                                                                                                                             No.:
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                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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Mammalian

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APPLICANT: HWANG, Inhwan
APPLICANT: KIM, Dae Heen
APPLICANT: LEE, Yong Jik
TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APBO2/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
CURRENT FILING DATE: 2002-08-08
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SEQ ID NO 51
                                                                                                                                                                                                                                      RESULT 32
US-10-214-932-51
j Sequence 51, Application US/10214932
j Publication No. US20030100707A1
j GENERAL INFORMATION:
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OTHER INFORMATION: S
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1638
OTHER INFORMATION: G
FEATURE:
                                                                     LENGTH: 1638
TYPE: DNA
ORGANISM: Artificial
PEATURE:
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             Gene
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             for
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             RFP:PS(NIa
                                                           Sequence
            protease):AtOEP7:GFP
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RESULT 33
US-10-214-932-75
; Sequence 75, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION:
; APPLICANT: HWANG, Inhwan
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Best Local Similarity:
Query Match:
DB:
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; NAME/KEY: misc feature
; OTHER INFORMATION: CDS: RFP(1..678); CDS: NIA protease proteolytic site(700..711); C
; OTHER INFORMATION: DS: AtOEP7(712..900); CDS: GFP(922..1635)
US-10-214-932-51
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Pred. No.:
Score:
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LOCATION: (1)..(1635)
OTHER INFORMATION: RFP:PS(NIa
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Matches:
Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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NAME/KEY: gene
LOCATION: (1)..(1647)
LOCATION: (1)..(1647)
OTHER INFORMATION: Gene for RFP:PS(HIV-1 protease):AtOEP7:GFP hybrid protein
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1644)
OTHER INFORMATION: RFP:PS(HIV-1 protease):AtOEP7:GFP hybrid protein
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: CDS: RFP(1..678); CDS: HIV-1 protease proteolytic site(700..720)
OTHER INFORMATION: CDS: AtOEP7(721..909); CDS: GFP(931..1644)
US-10-214-932-75
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APPLICANT: LEE, Yong Jik
TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APB02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1647
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Sequence
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                                                                                     | MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                                                                                              GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
 ATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC 543
                   IleH1sLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                                                                                                                                                                           GACGGCGGCGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
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APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 4692
TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-161-403-29
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
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   LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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Query Match:
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; OTHER INFORMATION: sequecne of vector pDsRed1-N1
US-10-433-640-16
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US-10-433-640-16
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LENGTH: 4692
TYPE: DNA
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Publication No. US20040115792A1

GENERAL INFORMATION:
APPLICANT: Lichtenberg-Frate, Hella
TITLE OF INVENTION: YEAST STRAIN FOR TESTING THE GENOTOXICITY AND CYTOTOXICITY OF
TITLE OF INVENTION: COMPLEX ENVIRONMENTAL CONTAMINATIONS
FILE REFERENCE: 1487/3
CURRENT APPLICATION NUMBER: US/10/433,640
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/14610
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-2-12
PRIOR FILING DATE: 2001-2-12
PRIOR FILING DATE: 2001-3-12
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HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60
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APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 17084-022002/420B
CURRENT APPLICATION NUMBER: US/11/006,076
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
SEQ ID NO 29
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Alignment Scores: Pred. No.: Score:
                                                                                  ; OTHER INFORMATION: pDSred1-N1 US-11-006-076-29
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APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
                                                                                                                                               LENGTH: 4692
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                               FEATURE:
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US-10-169-050-46
; Sequence 46, Application US/10169050
; Publication No. US20050071891A1
; GENERAL INFORMATION:
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APPLICANT: WIGNARAJAN, SOMA
APPLICANT: VIGNARAJAN, SOMA
APPLICANT: PATIL, JAMAHAR
APPLICANT: PATIL, JAMAHAR
TITLE OF INVENTION: REPRESSIBLE STERILITY OF ANI
FILE REFERENCE: 4050.001500
CURRENT APPLICATION NUMBER: US/10/169,050
CURRENT APPLICATION NUMBER: 2002-06-24
PRIOR APPLICATION NUMBER: PCT/AU00/0
PRIOR FILING DATE: 2000-12-22
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US-10-006-922A-12 (1-225) x US-10-169-050-46 (1-5436)
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PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 5436
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OTHER INFORMATION: pSFM6
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ORGANISM: Artificial Sequence
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LENGTH: 6984
TYPE: DNA
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
APPLICANT: BEAM, TERESA
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TITLE OF INVENTION: MITHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MITHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: WICTOR PIGGYBAC
TITLE OF INVENTION: VECTOR PIGGYBAC
FILE REFERENCE: 835910-92098
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR PILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
SOFTMARE: Patentin Ver: 2.1
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OTHER INFORMATION:
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TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp 200
                                                          IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
                                                                                                                                    MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
                                                                                                                                                                                       AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACC
                                                                                                                                                                                                          LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
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                                                                                                                                                                                                                                                                                                                                          GACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
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                                                                                                              ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
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1210.00
100.00%
99.56%
99.67%
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Matches:
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APPLICANT: VIGNARAJAN, SOMA
APPLICANT: GREWE, PETER MARTIN
APPLICANT: PATIL, JAMAHAR
ITITLE OF INVENTION: REPRESSIBLE STERILITY OF ANIMALS
FILE REFERENCE: 4050.001500
CURRENT APPLICATION NUMBER: US/10/169,050
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: PCT/AU00/0
PRIOR APPLICATION NUMBER: PCT/AU00/0
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-13-24
PRIOR FILING DATE: 19
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: HINDS, LYN
APPLICANT: HARDY, CHRIS
APPLICANT: WHYARD, STEVE
APPLICANT: VIGNARAJAN, SC
APPLICANT: VIGNARAJAN, SC
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AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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Conservative:
Mismatches:
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Sequence 20, Application US/10471065
Publication No. US20040197855A1
GENERAL INFORMATION:
APPLICANT: Prof. Dr. Wiesmueller, Lisa
TITLE OF INVENTION: Test system for the determination of
FILE REFERENCE: P59532
FILE REFERENCE: P59532
CURRENT APPLICATION NUMBER: US/10/471,065
CURRENT FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
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US-10-471-065-20
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NAME/KEY: promoter
LOCATION: (2267)...(2848)
OTHER INFORMATION: CMV promoter from the information of the information; (3348)
OTHER INFORMATION: (Clontech, Pale FEATURE:
                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)..(1592)
OTHER INFORMATION: Retroviral versions feature
LOCATION: (3374)..(3392)
OTHER INFORMATION: Retroviral versions feature
LOCATION: (527)..(9320)
OTHER INFORMATION: Retroviral versions feature
LOCATION: (5527)..(9320)
OTHER INFORMATION: Retroviral versions feature
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of the artificial sequence: OTHER INFORMATION: p5-Puro-CMV-(N'-EGFP)-CMV-Red-(EGFP-EJ) FEATURE:
                                                                                                                                                               NAME/KEY: gene
LOCATION: (1617)...(2216)
OTHER INFORMATION: Puromycin resistance gene
OTHER INFORMATION: Palo Alto, CA, USA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                  EGFP
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                  P from
USA)
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (4766)..(5
; OTHER INFORMATION: E
; OTHER INFORMATION: (1)
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LOCATION: (3411)..(3992)
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LOCATION: (4038)..(4718)
OTHER INFORMATION: Red from
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                                             HisHisLeuPheLeu
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                       CACCACCTGTTCCTG
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US-10-609-019-4
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PRIOR FILLING DATE: 2003-01-21
PRIOR PELLOATION NUMBER: US 60/441,377
PRIOR FILLING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/441,502
PRIOR APPLICATION NUMBER: US 60/441,405
PRIOR APPLICATION NUMBER: US 60/441,405
PRIOR APPLICATION NUMBER: US 60/441,405
PRIOR APPLICATION NUMBER: US 60/441,447
PRIOR APPLICATION NUMBER: US 60/441,447
PRIOR APPLICATION NUMBER: US 60/441,381
PRIOR APPLICATION NUMBER: US 60/441,381
PRIOR FILLING DATE: 2003-01-21
PRIOR FILLING DATE: 2003-01-21
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APPLICANT: DeBoor, Kenneth F.
APPLICANT: DeBoor, Kenneth F.
TITLE OF INVENTION: Gene Regulation in Transgenic Animals Using a Transposon-Based TITLE OF INVENTION: Vector
FILE REFERENCE: 51687-0101 (51687-287015)
CURRENT APPLICATION NUMBER: US/10/609,019
CURRENT FILING DATE: 2003-06-26
PRIOR APPLICATION NUMBER: US 60/392,415
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
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SOFTWARE: PatentIn version 3.2
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ORGANISM: Artificial Sequence
FEATURE:
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LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr 140
                                                                     AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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                                          GACGGCGGCGTGGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTAC
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; OTHER INFORMATION: Synthetic US-10-609-019-3
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PRIOR FILING DATE: 2002-06-26
PRIOR PELICATION NUMBER: US 60/441,392
PRIOR APPLICATION NUMBER: US 60/441,392
PRIOR FILING DATE: 2003-01-21
PRIOR PELICATION NUMBER: US 60/441,377
PRIOR PELICATION NUMBER: US 60/441,502
PRIOR PELICATION NUMBER: US 60/441,502
PRIOR PELICATION NUMBER: US 60/441,405
PRIOR APPLICATION NUMBER: US 60/441,405
PRIOR PILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/441,405
PRIOR PILING DATE: 2003-01-21
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PRIOR FILING DATE: 2003-01-21
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Publication No. US20040197910A1
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APPLICANT: Cadd, Gary G.
APPLICANT: Cadd, Gary G.
APPLICANT: Fioretti, William C.
APPLICANT: DeBoer, Kenneth F.
TITLE OF INVENTION: Gene Regulation in Transgenic Animals Using
TITLE OF INVENTION: Vector
FILE REFERENCE: 51687-0101 (51687-287015)
CURRENT APPLICATION NUMBER: US/10/609,019
CURRENT FILING DATE: 2003-06-26
CURRENT FILING DATE: 2003-06-26
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Sequence 2. Application US/10609019

Publication No. US20040197910A1

GENERAL INFORMATION:

APPLICANT: Cooper, Richard K.

APPLICANT: DeBoer, Kenneth F.

TITLE OF INVENTION: Gene Regulation in Transgenic Animals Using a Transposon-Based TITLE OF INVENTION: Vector

FILE REFERENCE: 51687-0101 (51687-287015)

CURRENT FILING DATE: 2003-06-26

PRIOR APPLICATION NUMBER: US 60/392,415

PRIOR APPLICATION NUMBER: US 60/392,415

PRIOR FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US 60/441,392

PRIOR APPLICATION NUMBER: US 60/441,397

PRIOR APPLICATION NUMBER: US 60/441,502

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PRIOR APPLICATION NUMBER: US 60/441,405
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       RESULT 44
US-10-315-920-3
; Sequence 3, Application US/10315920
; Publication No. US20030175809A1
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NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
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GENERAL INFORMATION:

AND METHODS

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APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND
TITLE OF INVENTION: FOR THEIR USE
FILE REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR PILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 3
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Pred. No.:
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ORGANISM: Artificial Sequence
FEATURE:
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IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                              TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp 200
                                                                                                        IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                                                                                                   MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
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US-10-742-828-4
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APPLICANT: Huynh, Gigi

TITLE OF INVENTION: TRANGENIC SCREEN AND ME
FILE REFERENCE: US 1353/03 (VA)

CURRENT APPLICATION NUMBER: US/10/742,828

CURRENT FILING DATE: 2003-12-23

PRIOR APPLICATION NUMBER: US 10/306,737

PRIOR FILING DATE: 2002-11-29
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SEQ ID NO 4
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TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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Matches:
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APPLICANT: LAKYANOV, Sergey A
APPLICANT: Fradkov, Arcady F.
APPLICANT: Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terskikh, Alexey
ITILE OF INVENTION: No. US20020197676Alel Chromophores and
ITILE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT APPLICATION NUMBER: 09/120,330
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/459,898
PRIOR APP
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US-10-006-922-37
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                                       HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60
                                                                                                                            ThrvalAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
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             CACAACACCGTGAAGCTGAAGGTGA
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Percent Similarity:
Best Local Similarity:
Query Match:
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; OTHER INFORMATION:
US-10-332-733-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 47
                                                            US-10-006-922A-12 (1-225) x US-10-332-733-22 (1-666)
                                                                                                                                                                  Score:
                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                             Sequence 22, Application US/10332733

Publication No. US20040106565A1

GENERAL INFORMATION:
APPLICANT: Margarate Odenthal and Diana Jung
APPLICANT: Margarate Odenthal and Diana Jung
TITLE OF INVENTION: Gene Expression, Genome Alteration And Reporter Expression
TITLE OF INVENTION: In Myofibroblasts And Myofibroblast-like Cells
FILLE REFERENCE: 1472/6806

CURRENT APPLICATION NUMBER: US/10/332,733
CURRENT APPLICATION NUMBER: US/10/332,733
CURRENT FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 41
SOFTWARB: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 666
TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                     FEATURE:
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               LyBASDVallleLySGluPheMetArgPheLySValArgMetGluGlyThrValAsDGly
Description Fluorescent
                                                                                                           1.25e-140
1196.00
100.00%
100.00%
98.52%
                                                                                                                                                                                                                                                   of artificial sequence: Protein
                                                                                                                Conservative: Mismatches: Indels:
                                                                                                                                                                  Length:
Matches:
                                                                                                  Gaps:
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HisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsnThrVal 44

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Sequence 1, Application US/10314936

Publication No. US20040110225A1

GENERAL INFORMATION:
APPLICANT: Glabbs, Patrick D.L.
APPLICANT: Carter, Robert W.
APPLICANT: Carter, Robert W.
APPLICANT: Schmale, Michael C.
TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
FILE REFERENCE: 638.004

CURRENT APPLICATION NUMBER: US/10/314,936

CURRENT FILING DATE: 2002-12-09

NUMBER OF SEQ ID NOS: 15

SOPTWARE: PatentIn version 3.1

SEQ ID NO 1
Score:
Percent Similarity:
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                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(711)
OTHER INFORMATION:
                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: mu
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   1.37e-140
1196.00
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Matches:
Conservative:
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                                           Sequence 3, Application US/10314936

Publication No. US20040110225A1

GENERAL INFORMATION:
APPLICANT: Gibbs, Patrick D.L.
APPLICANT: Carter, Robert W.
APPLICANT: Schmale, Michael C.
TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPEFILE REPERSINCE: 638.004
CURRENT APPLICATION NUMBER: US/10/314,936
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 711
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DB:
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    TYPE: DNA
ORGANISM: Artificial
FEATURE:
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US-11-021-014-1
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Sequence 1, Application US/11021014
Publication No. US20050100954A1
GENERAL INFORMATION:
APPLICANT: Gibbs, Patrick D.L.
APPLICANT: Carter, Robert W.
APPLICANT: Schmale, Michael C.
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NAME/KEY: CDS
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SEQ ID NO 1
LENGTH: 711
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NAME/KEY: CDS
LOCATION: (1)..(711
OTHER INFORMATION:
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FILE REFERENCE: 638.004
CURRENT APPLICATION NUMBER: US/11/021,014
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: US/10/314,936
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 15
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Publication No. US20050100954A1
GENERAL INFORMATION:
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SEQ ID NO 3
LENGTH: 711
TYPE: DNA
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APPLICANT: Garter, Robert W.
APPLICANT: Schmale, Michael C.
APPLICANT: Schmale, Michael C.
TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
FILE REFERENCE: 638.004
CURRENT APPLICATION NUMBER: US/11/021,014
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: US/10/314,936
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 15
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-035CLP
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/459,477
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR APPLICATION NUMBER: 09/444,338
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US-10-006-922-36
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APPLICANT: Fradkov, Arcady
APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Discosoma
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                                                                ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGC 120
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Matz, Mikhail V.
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Matches:
Conservative:
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APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushevich, Yuriy
APPLICANT: Savistky, Alexandr
APPLICANT: Savistky, Alexandr
APPLICANT: Savistky, Alexandr
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT APPLICATION NUMBER: 10/006,922
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 678
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US-10-081-864-14
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                          OTHER INFORMATION: non-aggregating US-10-081-864-14
                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/10081864
Publication No. US20030022287A1
GENERAL INFORMATION:
                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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 Length:
Matches:
Conservative:
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 FILE REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 678
TYPE: DNA
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US-10-315-920-5
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                                                                                                                                                                                           APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS
TITLE OF INVENTION: FOR THEIR USE
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Sequence 38, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey A
APPLICANT: Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terskikh, Alexey
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; OTHER INFORMATION: variant of
US-10-315-920-5
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TITLE OF INVENTION: No. US20020197676A1el Chromophores And TITLE OF INVENTION: Methods for Using the Same FILE REFERENCE: CLON-035CIP CURRENT APPLICATION NUMBER: US/10/006,922 CURRENT APPLICATION NUMBER: US/10/006,922 CURRENT FILING DATE: 2001-12-04 PRIOR FILING DATE: 1998-12-11 PRIOR PELICATION NUMBER: 09/120,330 PRIOR FILING DATE: 1998-12-11 PRIOR APPLICATION NUMBER: 09/457,898 PRIOR APPLICATION NUMBER: 09/457,898 PRIOR APPLICATION NUMBER: 09/45,144 PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/458,477 PRIOR APPLICATION NUMBER: 09/458,477 PRIOR APPLICATION NUMBER: 09/459,756 PRIOR APPLICATION NUMBER: 09/459,756 PRIOR APPLICATION NUMBER: 09/457,556 PRIOR APPLICATION NUMBER: 09/44,338 PRIOR FILING DATE: 1999-11-19 NUMBER: 09/544,338 PRIOR FILING DATE: 1999-11-19 NUMBER: 09/544,338
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; ORGANISM: Discosoma
US-10-006-922-38
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                                                       ACCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATC
                                                                            IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushevich, Yuriy
APPLICANT: Yanushevich, Yuriy
APPLICANT: Yanushevich, Yuriy
APPLICANT: Savistky, Alexandr
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. U$20030022287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067
CURRENT APPLICATION NUMBER: U$/10/081,864
CURRENT APPLICATION NUMBER: 10/006,922
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR FILING DATE: 2001-02-21
NUMBER: OF SEQ ID NOS: 30
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 675
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: non-aggregating mutant
US-10-081-864-13
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US-10-081-864-13
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Publication No. US20030022287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushevich, Yuriy
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                   AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                     AspTyrLysLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                               CTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCC
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Publication No. US20040261149A1

GENERAL INFORMATION:

APPLICANT: Donald Danforth Plant Science Center

APPLICANT: Fauquet, Claude M.

APPLICANT: Padmanabhan, Chellappan

APPLICANT: Ramachandran, Vanitharani

TITLE OF INVENTION: SIRNA-mediated inhibition of

FILE REFERENCE: C35621/104850

CURRENT APPLICATION UNUMBER US/10/785,862

CURRENT PILING DATE: 2004-02-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 747
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Best Local Similarity:
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ORGANISM: Artificial Sequence
FEATURE:
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                     LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAllaAspIlePro 80
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Query Match:
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; ORGANISM: Coral
US-10-060-857-7
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APPLICANT: Zhao, Ming
APPLICANT: Jiang, Ming
APPLICANT: Jiang, Ping
APPLICANT: Xu, Mingxu
APPLICANT: Yang, Meng
TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
FILE REFERENCE: 31276-20032.00
CURRENT APPLICATION NUMBER: US/10/060,857
CURRENT APPLICATION NUMBER: US/060,857
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/264,932
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 9
                                                                                                                                      US-10-006-922A-12 (1-225) x US-10-060-857-7 (1-1050)
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Pred. No.:
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US-10-060-857-7
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                                                                        ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
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              ACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCCGAGGGCCCCCTACGAGGGC
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Publication No. US20050130919A1
GENERAL INFORMATION:
APPLICANT: Xi, Zuoshang
APPLICANT: Xi4, XUGANG
TITLE OF INVENTION: REGULATABLE PROMOTERS FOR SYIFILE REFERENCE: UMY-072
CURRENT APPLICATION NUMBER: US/10/894,949
CURRENT ETLING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/488,510
PRIOR FILING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
Score:
Percent Similarity:
Best Local Similarity:
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                                                            Pred. No.:
                                                                        Alignment Scores:
                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 528, 2516
; OTHER INFORMATION: n =
US-10-894-949-9
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US-10-894-949-9
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                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                      TYPE: DNA
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Matches:
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Mismatches:
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948 220 888 200 828

SMALL HAIRPIN

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Sequence 8, Application US/10894949

Publication No. US20050130919A1

GENERAL INFORMATION:
APPLICANT: Xu, Zuoshang
APPLICANT: Xu, Zuoshang
APPLICANT: Xi, Xugang
ITILE OF INVENTION: REGULATABLE PROMOTERS FOR SYNTHESIS OF SMALL HAIRPIN RNA
FILE REFERENCE: UMY-072
CURRENT APPLICATION NUMBER: US/10/894,949

CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/488,510
PRIOR FILING DATE: 2003-07-18

NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8
LENGTH: 4300
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ORGANISM: Artificial Sequence FEATURE:
                           TYPE: DNA
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, NAME/KEY: misc feature
; LOCATION: 536, 2369
; OTHER INFORMATION: n = A,T,
US-10-894-949-8
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 Sequence 5, Application US/10742828
Publication No. US20040157294A1
GENERAL INFORMATION:
APPLICANT: Heinrich, Gerhard
APPLICANT: Huynh, Gigi
TITLE OF INVENTION: TRANSGENIC SCREEN AND METHOD FOR SCREENING MODULATORS OF BRAIN-DEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: expression construct
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; FILE REFERENCE: US 1353/03 (VA)
; CURRENT APPLICATION NUMBER: US/10/742,828
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 10/306,737
; PRIOR FILING DATE: 2002-11-29
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 7495
TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; NAME/KEY: Unsure
; OTHER INFORMATION: Synthesized
US-10-742-828-5
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Sequence 5, Application US/10510363

Publication No. US20050158724A1

GENERAL INFORMATION:
APPLICANT: Fishel, Richard A.
APPLICANT: Yoder, Kristine E.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE A DNA REPAIR
TITLE OF INVENTION: PATHWAY AND/OR RETRO-VIRAL INFECTIVITY, THE COMPOUNDS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SCHN-0033
CURRENT APPLICATION NUMBER: US/10/510,363
CURRENT FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: PCT/US03/10302
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.3
SEQ ID NO 5
LENGTH: 9731
TYPE: DNA
CRGANISM: Artificial
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Best Local Similarity:
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US-10-510-363-5
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OTHER INFORMATION:
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                 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                                    MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu
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; OTHER INFORMATION: Synthesized retroviral vectors
US-10-510-363-6
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Pred. No.:
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Publication No. US20050158724A1
GENERAL INFORMATION:
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SEQ ID NO 6
LENGTH: 9782
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APPLICANT: Yoder, Kristine E.
APPLICANT: Yoder, Kristine E.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE A DNA REPAIR
TITLE OF INVENTION: METHODS OF IDENTIFYING TIPECTIVITY, THE COMPOUNDS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: SCHN-0033
CURRENT APPLICATION NUMBER: US/10/510,363
CURRENT FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: PCT/US03/10302
PRIOR APPLICATION NUMBER: US/60/370,376
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2002-04-05
PRIOR PRI
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                                    AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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APPLICANT: LIAVANOV, Sergey A
APPLICANT: LIAVANOV, Arcady F.
APPLICANT: LIAVANOV, Arcady F.
APPLICANT: LIAVANOV, Arcady F.
APPLICANT: LIAVANOV, Sergey A
APPLICANT: LIAVANOV, Sergey A
APPLICANT: Terskikh, Alexey
ITILE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
ITILE OF INVENTION: Methods for Using the Same
ITILE OF INVENTION: MUMBER: 09/120,330
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/459,556
PRIOR APPLICATION NUMBER: 09/459,556
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-11-19
SOPTWARE FASTSEQ for Windows Version 4.0
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US-10-006-922-45
; Sequence 45, Application US/10006922
; Publication No. US20020197676A1
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Best Local Similarity:
Query Match:
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                                                                                                            US-10-006-922A-12 (1-225) x US-10-006-922-45 (1-898)
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TYPE: DNA
ORGANISM: Discosoma
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97.53%
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APPLICANT: Talien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND METHODS FOR MAK
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FABESEQ for Windows Version 4.0
                               ; OTHER INFORMATION: ; OTHER INFORMATION: US-10-121-258-5
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US-10-121-258-5
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 Alignment Scores
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                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Sequence 5, Application US/10931304;
Publication No. US20050196768A1

GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Tsien, Roger
ITILE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
ITILE OF INVENTION: MONOMERIC AND METHODS FOR MAI
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/1209,208
PRIOR APPLICATION NUMBER: 10/1201,258
PRIOR APPLICATION NUMBER: 10/121,258
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Best Local Similarity:
Query Match:
DB:
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US-10-931-304-5
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
COTHER INFORMATION: Polynucleotide encoding DsRed polypeptide variant
OTHER INFORMATION: "TI"
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PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
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               HisHisLeuPheLeu 225
                                                                 IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
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Sequence 3, Application US/10844064A

publication No. US20050149994A1

publication No. US20050149994A1

general information:
APPLICANT: Bevis, Brooke
APPLICANT: Bevis, Brooke
FAPLICANT: Glick, Benjamin
FILLE OF INVENTION: RAPIDLY MATURING FLUORESCENT PROTEINS AND
FILE REFERENCE: 092234-9006

CURRENT APPLICATION UNMBER: US/10/844,064A

CURRENT APPLICATION UNMBER: PCT/US02/40539

PRIOR APPLICATION NUMBER: PCT/US02/40539

PRIOR APPLICATION NUMBER: US 60/341,723

PRIOR APPLICATION NUMBER: US 60/341,723

PRIOR APPLICATION NUMBER: US 60/341,723

PRIOR FILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 3

PRIOR FILING DATE: 2001-12-19
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SEQ ID NO 3
SEQ ID NO 3
SENGTH: 704
TYPE: DNA
ORGANISM: Discosoma
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                                             11eHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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                                                                                               ATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAG
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US-10-423-688A-40
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Pred. No.:
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APPLICANT: Waldo, Geoffrey S.
TITLE OF INVENTION: Directed Evolution Methods for Improving Polypeptide Folding and
TITLE OF INVENTION: Solubility and Superfolder Fluorescent Proteins Generated Thereb
FILE REFERENCE: S-100,608
CURRENT PEPLICATION NUMBER: US/10/423,688A
CURRENT FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: 10/132,067
PRIOR APPLICATION NUMBER: 10/132,067
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/10423688A Publication No. US20040078148A1 GENERAL INFORMATION:
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                            MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                         Ly6ValLy6PheIleGlyValAsnPheProSerAspGlyProValMetGlnLy6Ly6Thr 140
                                                                                                                           AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
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                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Polynucleotide
OTHER INFORMATION: "dimer2"
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                              190
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                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAM:
FILLE REFERENCE: UCO83.1CP2CP1
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 681
                                                                                                                            AsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsn 42
                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCCGAGGACGTCATCAAAGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCTCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGly 102
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                                                                                                                                                                                                                                         ThrVallysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSer 62
                                                                                                                                                                                                                                                                                                             AACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCCCTACGAGGGCACCCAG
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Sequence 7, Application US/10931304
; Publication No. US20050196768A1
; Publication No. US20050196768A1
; Publication No. US20050196768A1
; Publication No. US20050196768A1
; Publicavi: Tsien, Roger
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; FILLE REFERENCE: 39754-0831CP2CP3
; CURRENT APPLICATION NUMBER: US/10/931,304
; CURRENT FLING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: 10/121,258
; PRIOR APPLICATION NUMBER: 10/121,258
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-05-26
; NUMBER OF SEQ ID NOS: 110
; SOPTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 7
; ERNCTH. 681
                                                                                                                                                                                                                       LENGTH: 681
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Artificial Sequence
; ORHER INFORMATION: Polynucleotide encoding DsRed polypeptide variant
; OTHER INFORMATION: "dimer2"
US-10-931-304-7
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US-10-931-304-7
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Pred. No.:
                                                            US-10-006-922A-12 (1-225) x US-10-931-304-7 (1-681)
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GlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysVal 122
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Matches:
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   69
                                                                                                                                           FILE REFERENCE: STAN-385
CURRENT APPLICATION NUMBER: US/11/052,001
CURRENT FILING DATE: 2005-02-03
PRIOR APPLICATION NUMBER: 60/541,297
PRIOR FILING DATE: 2004-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1809
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                     Pred. No.:
                                 Alignment Scores
                                                                 ; OTHER INFORMATION: US-11-052-001-5
                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/11052001
Publication No. US20050233356A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         APPLICANT: JONES, JOSHUA T.
APPLICANT: HAHN, ANGELA TERESA
APPLICANT: MEYER, TOBLAS
TITLE OF INVENTION: LIVE-CELL BIOSENSOR POLYPEPTIDES
TITLE OF INVENTION: METHODS OF USE
                                                                                                 ORGANISM: Artificial FEATURE:
                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuPheLeu
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                                                                                  expression
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   1.47e-130
1121.00
      Length:
Matches:
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609

249

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RESULT 72

US-10-006-922-43
; Sequence 43, Application US/10006922
; Publication No. US20020197676A1
; Dablication No. US20020197676A1
; APPLICANT: Likyanov, Sergey A
; APPLICANT: Likyanov, Sergey F.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Terskith, Alexey
TITLE OF INVENTION: No. US20020197676A1e1 Chromophores and
; TITLE OF INVENTION: Methods for Using the Same
; TITLE REFERENCE: CLON-035CIP
; CURRENT APPLICATION NUMBER: US/10/006,922
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR APPLICATION NUMBER: 09/457,898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGTGGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCACGCTGATCTACAAGGTG
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Best Local Similarity:
Query Match:
DB:
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PRIOR APPLICATION NUMBER: 09/458,144
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-12-09
PRIOR PLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 4.
ENGTH: 678
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                           CGGGGCTGGGAGGCAGCAGCGAGCGAGCGACCCCGGGACGGCGTGCTCAAGGGCGAC
                                                                                                                                                                                                             MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                                                                                                                          CTCAGCCCCCAGTTCCAGTACGGCAGCCAGCGTGAAGCACCCCGCCGACATCCCC
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                                      IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                                                                                    ATCCACATGGCCCTCCGGCTCGAGGGCGGCGGCCACTACCTCGTGGAGTTCAAGAGCATC
                                                                                                                                                      eHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle 180
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Matches:
Conservative:
Mismatches:
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APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushevich, Yuriy
APPLICANT: Savistky, Alexandr
APPLICANT: Savistky, Alexandr
APPLICANT: Pradkov, Arcady
ITILE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
ITILE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hybrid coding sequence
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Best Local Similarity:
Query Match:
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US-10-081-864-11
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MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                                                                                       AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu 100
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                                                                         LygValLygPheIleGlyValAgnPheProSerAspGlyProValMetGlnLygLygThr
                                                                                                                                     AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                    GACTACAAGAAGCTCAGCTTCCCCGAGGGCTTCAAGTGGGAGCGGGTGATGAACTTCGAG
                                                     GAGGTGAAGTTCATCGGCGTGAACTTCCCCAGCGACGGCCCCGTGATGCAGCGGCGGACC
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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND METHODS FOR MAKING SAME
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR PILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Polynuc. of Polypeptide variant "dimer2.2MMM(dimer3)(dtomato)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                     136
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                                                                           45 LysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSerProGln
                                                                                                                       76 CACGAGTTCGAGATCGAGGGCGAGGGCCGAGGGCCCCTACGAGGGCACCCAGACCGCC 135
                                                                                                                                             25 HisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsnThrVal 44
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PheGlnTyrGlySerLysValTyrValLysHisProAlaAspIleProAspTyrLysLys
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APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC VARIANTS AND METHODS FOR MAK
FILE REFERENCE: 39754-0831CP2CP3
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/21,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/966,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 107
LENGTH: 1431
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide encoding DsRed polypep
                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                    Score:
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US-10-931-304-107
; Sequence 107, Application US/10931304
; Publication No. US20050196768A1
; GENERAL INFORMATION:
                                                                                                                    Alignment Scores:
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APPLICANT: Campbe
APPLICANT: Baird,
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Matches:
Conservative:
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Sequence 17, Application US/10006922

| Publication No. US20020197676A1
| GENERAL INFORMATION:
| APPLICANT: Lityanov, Sergey A
| APPLICANT: Fradkov, Arcady F.
| APPLICANT: Labas, Yulii A.
| APPLICANT: Habas, Yulii A.
| APPLICANT: Matz, Mikhail V.
| APPLICANT: Terekikh, Alexey
| TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
| TITLE OF INVENTION: Methods for Using the Same
| TITLE OF INVENTION UNMBER: US/10/006,922
| CURRENT APPLICATION NUMBER: US/10/006,922
| CURRENT APPLICATION NUMBER: 09/457,898
| PRIOR APPLICATION NUMBER: 09/457,898
| PRIOR APPLICATION NUMBER: 09/458,144
| PRIOR APPLICATION NUMBER: 09/458,477
| PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                       RESULT 76
US-10-006-922-17
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Percent Similarity:
Best Local Similarity:
Query Match:
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TYPE: DNA
ORGANISM: Discosoma
US-10-006-922-17
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RESULT 77
US-10-161-403-39
; Sequence 39, A
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PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                       525
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  39, Application US/10161403
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Matches:
Conservative:
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Indels:
Gaps:
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APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
APPLICANT: Shellard, Joan
APPLICANT: Shellard, Joan
APPLICANT: Shellard, Joan
CURRENT EPPLICATION NUMBER: US/10/161,403
CURRENT APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR PILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
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APPLICANT: Perkins, Edwa
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20030119104A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Discosoma species
FEATURE:
NAME/KEY: CDS
LOCATION: (45)...(737)
OTHER INFORMATION: Nucleotide sequence encoding red
OTHER INFORMATION: protein (FP593)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AF272711
DATABASE ENTRY DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 876
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MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
                                                                                                                                            AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                                                                                            AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
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                                                          LysValLysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThr
                                                                                                              GACGGTGGCGTGGTTACTGTATCCCAAGATTCCAGTTTGAAAGACGGCTGTTTCATCTAC
                                                                                                                                                                                    GACTATAAAAAGCTGTCATTTCCTGAGGGATTTAAATGGGAAAGGGTCATGAACTTTGAA
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                                      GAGGTCAAGTTCATTGGGGTGAACTTTCCTTCTGATGGACCTGTTATGCAGAGGACGACA
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1085.50
95.58%
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Matches:
Conservative:
Mismatches:
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APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 17084-022002/420B
CURRENT APPLICATION NUMBER: US/11/006,076
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2002-03-21
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Discosoma species
FEATURE:
NAME/KEY: CDS
LOCATION: (45)...(737)
OTHER INFORMATION: Nucleotide sequence encoding red flourescent
OTHER INFORMATION: protein (FP593)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Perkins, Edw
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum,
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Leung, Josephine
Fleming, Elena
Stewart, Sandra
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                                                                                               MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly
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                 ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
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US-10-724-178-15
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APPLICANT: Odyssey Thera, Inc.
APPLICANT: Michnick, Stephen
APPLICANT: MacDonald, Marnie
APPLICANT: Lamerdin, Jane
TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS
TITLE OF INVENTION: COMPLEMENTATION ASSAYS
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/461,133
PRIOR FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/10724178 Publication No. US20040137528A1
             NAME/KEY: CDS
LOCARTION: (1)..(675)
LOCARTION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Campbell, R.E. et al
TITLE: A monomeric red fluorescent
JOURNAL: Proc. Nat'l. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ODDY007
CURRENT APPLICATION NUMBER: US/10/724,178
CURRENT FILING DATE: 2003-12-01
                                                                                                                                                     FEATURE: OTHER INFORMATION: "mRFP1",
                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial
   VOLUME: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645
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; ISSUE: 12
; PAGES: 7877-82
; DATE: 2002-06-11
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US-10-121-258-9
Sequence 9, Application US/10121258
Publication No. US20030059835A1
GENERAL INFORMATION:
APPLICANT: Teien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING
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; TYPE: DNA
; ORGANISM: Artificial s
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CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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                                                                                                        TyrMetAlaLysLysProValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAsp
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ATCACCTCCCACAACGAGGACTACACCATCGTGGAACAGTACGAGCGCCGCCGAGGGCCGC
                    | IleThrSerHisAsnGluAspTyrThrIleValGluGlnTyrGluArgThrGluGlyArg
                                                                            TACATGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAAGACCGACATCAAGCTGGAC
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GENERAL INFORMATION:

APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
ITILE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
ITILE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
ITILE OF INVENTION: MONOMERIC US/10/931,304
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR FILING DATE: 2001-05-40
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-26
NUMBER OF SEQ ID NOS: 110
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Publication No. US20050196768A1
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                                                                                                                                                                                                                                                                                              ACCCAGACCGCCAAGCTGAAGGTGACCAAGGGCGGCCCCTGCCCTTCGCCTGGGACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetArgSerSerLysAsnValIleLysGluPheMetArgPheLysValArgMetGluGly
                      Ly6ValLy8PheIleGlyValA6nPheProSerA6pGlyProValMetGlnLy6Ly8Thr 140
                                                                                       AspG1yG1yVa1Va1ThrVa1ThrG1nAspSerSerLeuG1nAspG1yCysPheI1eTyr
                                                                                                                                               GACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                                                    AspTyrLysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGlu
                                                                                                                                                                                                                     CTGTCCCCTCAGTTCCAGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCC
                                                                                                                                                                                                                                          LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro
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<u>AAGGTGAAGCTGCGCGCACCAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACC</u>
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1021.00
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Matches:
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US-10-931-304-109
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DB:
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Best Local Similarity:
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CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ
SEQ ID NO 109
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APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-02-26 NUMBER OF SEQ ID NOS: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 39754-0831CP2CP3
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Polynucleotide encoding DsRed polypeptide variant "mGrapel'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                     HisAsnThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIle 60
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                                                                                                                                         ATGGCCTCCTCCGAGGACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
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o. US20050196768A1
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Matches:
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APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC PLUGRESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAK
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-0
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/86,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 80
SEQ ID NO 80
TYPE: DNA
ORGANISM: Artificial Sequence
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Percent Similarity:
Best Local Similarity:
                                                                    Pred. No.:
                                                                                          Alignment Scores:
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                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Polynucleo
OTHER INFORMATION: "mRFP1.1"
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No. US20050196768A1
                                                                                                                                                                 Polynucleotide encoding DsRed polypeptide variant "mRFP1.1"
    2.15e-117
1012.00
88.69%
85.97%
       Length:
Matches:
Conservative:
Mismatches:
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       APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FL
TITLE OF INVENTION: PROTEIN VARIANTS AND ME
TIER REFERENCE: 39754-0831CP2CP3
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2002-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
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PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOPTWARE: FastSEQ for Windows Ve
SEQ ID NO 105
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
RESULT 85
US-10-931-304-101
; Sequence 101, Application US/10931304
; Publication No. US20050196768A1
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Conservative:
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GENERAL INFORMATION:

APPLICANT: Tsien, Roger

APPLICANT: Campbell, Robert

APPLICANT: Baird, Geoffrey

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLU

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLU

TITLE OF INVENTION: MONOMER: US/10/931,304

FILE REFERENCE; 39754 0831CP2CP3

CURRENT APPLICATION NUMBER: US/10/931,304

CURRENT FILING DATE: 2004-08-30

PRIOR APPLICATION NUMBER: 10/121,258

PRIOR FILING DATE: 2002-04-10

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: 09/944,308

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 110

SEQ ID NO 101

SEQ ID NO 101

SEQ ID NO 101

LENGTH: 678

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Polynucleotide encoding

US-10-931-304-101
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly
                                                                                                                                                                                                      AspGlyGlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyr 120
                                                                                                                                                                                                                                                      GACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAG
                                                                                                                                                                                      GACGGCGGCGT
                                                                                                                                                                                                                                                                                                                        CTGTCCCCTCAGTTCTGTTACGGCTCCAAGGCCTACGTGAAGCACCCCGGCGACATCCCC
IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
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1002.00
88.24%
85.52%
82.54%
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Matches:
Conservative:
Mismatches:
Indels:
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METHODS FOR
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**ATCAAGATGAGGCTGAAGCTGAAGGACGGCGGCCACTACGACGCCGAGGTCAAGACCACC** 

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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-931-304-86
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OTHER INFORMATION: Polynucleotide encoding US-10-931-304-86
                                                                                                                                                                                                                                                                                                                                                   US-10-006-922A-12 (1-225) x US-10-931-304-86 (1-711)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 10/209/208
PRIOR FILING DATE: 2002-07-29
PRIOR PELICATION NUMBER: 10/121,258
PRIOR PELICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/966,538
PRIOR PILING DATE: 2001-05-24
PRIOR PELICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Ro
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LENGTH: 711
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Baird, Geoffrey
TITLE OP INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OP INVENTION: MONOMERIC AND METHODS FOR MAKING SAME
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
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                                                                                                                                                                                                                              PheGluIleGluGlyGluGlyArgProTyrGluGlyHisAsnThrValLysLeu
                                                                                   TyrGlySerLysVallyrValLysHisProAlaAspIleProAspTyrLysLysLeuSer
                                                                                                                                                          LysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSerProGlnPheGln
             PheProGluGlyPheLy8TrpGluArgValMetABnPheGluAspGlyGlyValValThr 106
                                                                                                                                   AAGGTGACCAAGGGTGGCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCACC
                                                                 TACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCCGACTACTTGAAGCTGTCC
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994.00
88.84%
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81.88%
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Matches:
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APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAMI
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/21,258
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
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US-10-931-304-90
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                                                                                                                                           US-10-006-922A-12 (1-225) x US-10-931-304-90 (1-711)
                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                    Alignment Scores: Pred. No.:
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; SEQ ID NO 90
TOMOTH: 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514
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                      PheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsnThrValLysLeu 46
                                                                      GTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCTCCGTGAACGGCCACGAG
                                                                                           VallleLysGluPheMetArgPheLysValArgMetGluGlyThrValAsnGlyHisGlu
   TTCGAGATCGAGGGCAAGGGCGAGGGCCCCTACGAGGGCACCCAGACCGCCAAGCTG
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No. US20050196768A1
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992.00
88.84%
86.05%
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Mismatches:
Indels:
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Matches:
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APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLI
TITLE OF INVENTION: PROTEIN VARIANTS AND MET
FILE REFERENCE: 39754-0831CPCCP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR PRILING DATE: 2001-05-26
NUMBER OF SEQ ID NOS: 110
SEQ ID NO 103
SEQ ID NO 103
LENGTH: 711
TANGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Polynucleotide encoding
 Percent Similarity:
Best Local Similarity:
Query Match:
                                                    Score:
                                                                                      Alignment Scores:
                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 88
US-10-931-304-103
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PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR PELLING DATE: 2002-04-10
PRIOR FILLING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILLING DATE: 2001-05-24
PRIOR PILLING DATE: 2001-02-26
NUMBER: 09/794,308
PRIOR FILLING DATE: 2001-02-26
NUMBER: 0F SEQ ID NOS: 110
SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 84
LENGTH: 711
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Publication No. US20050196768A1
GENERAL INFORMATION:
APPLICANT: Telen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR
FILE REFERENCE: 39754-0831CP2CP3
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CURRENT FILING DATE: 2004-08-30
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Sequence 93, Application US/10931304
Publication No. US20050196768A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROFEIN VARIANTS AND METHODS FOR MAI
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
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PRIOR APPLICATION NUMBER: 10/209,208
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR PILING DATE: 2001-05-26
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FRASTSEQ for Windows Version 4.
SEQ ID NO 93
LENGTH: 711
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Best Local Similarity:
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ORGANISM: Artificial Sequence
FEATURE:
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GACTACACCATCGTGGAACAGTACGAACGCGCCGAGGGCCGCCAC
                     AspTyrThrIleValGluGlnTyrGluArgThrGluGlyArgHis
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-931-304-95

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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUGRESCENT
TITLE OF INVENTION: MONOMERIC NOT METHODS FOR MAI
FILE REFERENCE: 39754-0831CPZCP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR PILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/666,538
PRIOR APPLICATION NUMBER: 09/966,538
PRIOR FILING DATE: 2001-05-24
PRIOR PILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
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Best Local Similarity:
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LENGTH: 708
TYPE: DNA
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Publication No. US20050196768A1
GENERAL INFORMATION:
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LOCATION: 185
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ThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLys 166
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Best Local Similarity:
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US-10-931-304-97
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PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 97
LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97, Application US/10931304
Publication No. US20050196768A1
GENERAL INFORMATION:
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APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR
FILE REFERENCE: 39754-0831CP2CP3
CURRENT APPLICATION NUMBER: US/10/931,304
CURRENT FILING DATE: 2004-08-30
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PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
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OTHER INFORMATION: Polynucleotide
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ORGANISM: Artificial Sequence
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PheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGlyGlyValValThr 106
                                                                                                             AAGGTGACCAAGGGTGGCCCCCTGCCCTTCGCCTGGGACATCCTAACCCCCAACTTCACC 213
                                                                                                                                                                                                       PheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsnThrValLysLeu 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspTyrThrIleValGluGlnTyrGluArgThrGluGlyArgHis 221
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                                   TACGGCTCCAAGGCCTACGTGAAGCACCCCGGCCGACATCCCCGACTACTTGAAGCTGTCC
                                                        TyrGlySerLysValTyrValLysHisProAlaAspIleProAspTyrLysLysLysLeuSer 86
                                                                                                                                LysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSerProGlnPheGln
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84.65%
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Matches:
Conservative:
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APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FIL
TITLE OF INVENTION: PROTEIN VARIANTS AND MEJ
FILE REFERENCE: 39754-0831CP2CP3
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/209,208
PRIOR APPLICATION NUMBER: 10/21,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/94,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NO5: 110
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 99
LENGTH: 711
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                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                    US-10-006-922A-12 (1-225) x US-10-931-304-99 (1-711)
                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                         Query
                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Applica publication No. US20 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAanPheProSerAapGlyProValMetGlnLysLysThrMetGlyTrpGluAlaSer 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlnLeuProGlyTyrTyrTyrValAspSerLysLeuAspIleThrSerHisAsnGlu
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                                                           ValIleLysGluPheMetArgPheLysValArgMetGluGlyThrValAsnGlyHisGlu
 PheGluIleGluGlyGluGlyArgProTyrGluGlyHisAsnThrValLysLeu 46
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No. US20050196768A1
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                                                                                                                                                                                                                             APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, Robert
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLI
TITLE OF INVENTION: PROTEIN VARIANTS AND MET
FILE REFERENCE: 39754-0831CP2CP3
FILE REFERENCE: 39754-0831CP2CP3
FILE REFERENCE: 2004-08-30
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 10/29,208
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/124,258
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-26
PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 94
US-10-931-304-88
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                          Alignment Scores:
Pred. No.:
                                                                           OTHER INFORMATION:
US-10-931-304-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 88, Application US/10931304
Publication No. US20050196768A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                               SEQ ID NO 88
LENGTH: 711
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version
                                                                                                              FEATURE:
                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                              Polynucleotide
                                                                                              of polypeptide variant "Y1.3(mYOFP 1.3)(mBanana)"
              Length:
Matches:
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METHODS FOR MAKING
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RESULT 95
US-10-724-178-1040
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                                            CURRENT APPLICATION NUMBER: US/10/724,178
CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: US 60/461,133
PRIOR FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: Patentin version 3.0
SEQ ID NO 1040
                                                                                                                                                                                                                                                                  Sequence 1040, Application US/10724178 Publication No. US20040137528A1 GENERAL INFORMATION:
                                                                                                                                                         APPLICANT: Odyssey Thera, Inc.
APPLICANT: Michnick, Stephen
APPLICANT: MacDonald, Marnie
APPLICANT: Lamerdin, Jane
TITLE OF INVENTION: COMPLEMENTATION ASSAYS
FILE REFERENCE: ODDY007
LENGTH: 549
TYPE: DNA
ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHisLysAlaLeuLys 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGlyTrpGluAlaSer 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysValLysPheIleGly 126
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LOCATION: (1)..(549)
OTHER INFORMATION: RFP
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                        AlaLys 184
                                                  ATGAGGCTGAAGCTGAAGGACGGCGGCCACTACGACGCCGAGGTCAAGACCACCTACATG
                                                                   LysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIleTyrMet 182
                                                                                                                    TrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHis 162
                                                                                                                                                          AAGCTGCGCGCACCAACTTCCCCCTCCGACGGCCCCGTAATGCAGAAGAAGAACCATGGGC
                                                                                                                                                                         LysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGly 142
                                                                                                                                                                                                              GGCGTGGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTG 363
                                                                                                                                                                                                                            GlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysVal 122
                                                                                                                                                                                                                                                                 TIGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGC 303
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                                                                                                                                                                                                                                                                                                                  CCTCAGTTCCAGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCCGGACTAC 243
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-Q-/cgn2 1/USPTO spool p/US10006922/runat_10012006 162506 19200/app_query.fasta_1.391
-DB=bublished Applications NA New -QFWT=fastap -SUFFIX=p2nminscr.rnpbn
-MINMATCH=0.1 -LCOPCL=0 -LCOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=500 -DCCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=69 -ALIGN=500 -MDDE=LCCAL -OUTFWT=pto -NORM-ext
-HEAFSIZE=500 -MINIEN=0 -MAXLEN=200000000
-USER-US10006922 @CGN 1 184 @runat 10012006 162506 19200 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN ITMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEVATT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2: /cgm2 6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgm2 6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgm2 6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

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6: /cgm2 6/ptodata/1/pubpna/US1_NEW_PUB.seq:*

7: /cgm2 6/ptodata/1/pubpna/US1_NEW_PUB.seq:*

8: /cgm2 6/ptodata/1/pubpna/US1_NEW_PUB.seq:*

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US-11-218-880-2

US-10-209-208-3

US-10-209-208-23

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                             241 GACTATAAAAGCTGTCATTTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACTTTGAA 300
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ALIGNMENTS  1 209-208-2 20	8 1186 97.7 7927 6 US-10-655-872-7 Sequence 7, Appli 9 1160 95.6 678 6 US-10-209-208-5 Sequence 5, Appli 10 1160 95.6 678 7 US-11-218-880-5 Sequence 5, Appli 11 1121 92.3 681 6 US-10-209-208-7 Sequence 7, Appli 12 1121 92.3 681 7 US-11-218-880-7 Sequence 7, Appli 13 1021 84.1 678 6 US-10-209-208-9 Sequence 9, Appli 14 1021 84.1 678 7 US-11-218-880-9 Sequence 9, Appli
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Sequence 2. Application US/11218880

Publication No. US20060003420A1

GENERAL INFORMATION:
APPLICANT: TSien, ROGET

APPLICANT: Campbell, Robert

TITLE OF INVENTION: MONOWERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAK

FILE REFERENCE: UC083.1CP2CP1

CURRENT APPLICATION NUMBER: US/11/218,880

CURRENT PILING DATE: 2005-09-01

PRIOR APPLICATION NUMBER: US/10/121,258

PRIOR FILING DATE: 2002-04-10

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEG ID NOS: 78

SOPTWARE: FASTSEQ for Windows Version 4.0

1 ENCRUP.
                                                                                                                                                                                                                                ; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp.
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(678)
; OTHER INFORMATION: wild-type Do
US-11-218-880-2
                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                        Score:
                                                                                     US-10-006-922A-12 (1-225) x US-11-218-880-2 (1-678)
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                               ATGAGGTCTTCCAAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGCATGGAAGGA
                                              MetArgSerSerLysAsnVall1eLysGluPheMetArgPheLysValArgMetGluGly 20
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Sequence 3, Application US/10209208

Publication No. US20050244921A1

GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
CURRENT INVENTION: FULORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.1CPCP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/121,258
PRIOR APPLICATION NUMBER: 09/121,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FRSTSEQ for Windows Version 4.0
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OTHER INFORMATION: nucleotide sequence encoding DsRed with OTHER INFORMATION: codon usage
                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                  LENGTH:
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RESULT 4

US-10-209-208-23

; Sequence 23, Application US/10209208

; Publication No. US20050244921A1

; GENERAL INFORMATION:
   APPLICANT: Teien, Roger
   APPLICANT: Campbell, Robert
   APPLICANT: Geoffrey Baird
   TITLE OF INVENTION: FUURESCENT PROTEIN VARIANTS AND TITLE OF INVENTION: FOR MAKING SAME
   TITLE OF INVENTION: US/10/209,208
   CURRENT APPLICATION NUMBER: US/10/209,208
   CURRENT APPLICATION NUMBER: 10/121,258
   PRIOR APPLICATION NUMBER: 10/121,258
   PRIOR FILING DATE: 2002-04-10
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PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTMARE: FASTSEQ for Windows Version 4.
SEQ ID NO 23
LENGTH: 681
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ORGANISM: Artificial Sequence
FEATURE:
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CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 681
TYPE DAA
ORGANISM: Artificial S
FEATURE:
OTHER INFORMATION: nuc
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APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR
FILE REFERENCE: UC083.1CP2CP1
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 IleHisLysAlaLeuLysLeuLysAspGlyGlyHisTyrLeuValGluPheLysSerIle
                                                                   MetGlyTrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGlu 160
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                                                                                                            AAGGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACC
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Percent Similarity:
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CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-05-24
NUMBER: OF SEQ ID NOS: 78
SOPTWARE: FASTSEQ for Windows Version 4.0
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TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING
FILE REFERENCE: UC083.1CP2CP1
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APPLICANT: Campbell,
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OTHER INFORMATION: nucleotide sequence encoding
OTHER INFORMATION: codon usage
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ORGANISM: Artificial Sequence
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                                                                                  LeuSerProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIlePro 80
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                                                                                                                                      CACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATC
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Sequence 4, Application US/10655872

; Deblication No. US20050251872A1
; GENERAL INFORMATION:
   APPLICANT: Bear, et al.
   TITLE OF INVENTION: Lentiviral Vectors, Related Reagents, and Methods of Use Ther
   TITLE REFERENCE: 0492611-0512
   CURRENT APPLICATION UNMER: US/10/655,872
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 6706
; TYPE: DNA
; ORGANISM: Artificial
; PEATURB:
; OTHER INFORMATION: lentiviral vector sequence
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Best Local Similarity:
Query Match:
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US-10-655-872-4
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Matches:
Conservative:
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APPLICANT: Testen, Roger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLOORESCENT PROTEIN VARIANTS AND
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC083.LCP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                        FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
US-10-209-208-5
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                                                                                                                       SEQ ID NO 5
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Teien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Campbell, ROSERT
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAI
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/11/218,880
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-209-208-7
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LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
Sequence 7, Application US/10209208
Publication No. US20050244921A1
GENERAL INFORMATION:
APPLICANT: Teien, Roger
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Percent Similarity:
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APPLICANT: Geoffrey Baird
ITITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND
ITITLE OF INVENTION: FOR MAKING SAME
FILL REFERENCE: UC083.LCP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/666,538
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-02-26
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OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerSerLysAsnVall1eLysGluPheMetArgPheLysValArgMetGluGlyThrVal
                                                                                                                                                                                                                        LysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGly
                                                                                                                                                                                                                                                                                                                                                             LysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGly 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSer
AlaLysLysProValGlnLeuProGlyTyrTyrValAspSerLysLeuAspIleThr 202
                                                                 CAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGACCATCTACATG
                                                                                        TrpGluAlaSerThrGluArgLeuTyrProArgAspGlyValLeuLysGlyGluIleHis
                                                                                                                                                                                                     AAGTTCCGCGGCACCAACTTCCCCCCCGACGGCCCCGTAATGCAGAAGAAGACCATGGGC
                                                                                                                                                                                                                                                                                                                                       AAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGC
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                                                                                                                                       TGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGCGTGCTGAAGGGCGAGATCCAC
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Matches:
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US-11-218-880-7
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
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APPLICANT: Campbell,
TITLE OF INVENTION: MONOMERIC AND DIMERIC
TITLE OF INVENTION: PROTEIN VARIANTS AND
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/11/218,880
CURRENT FILING DATE: 2005-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 681
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                               310
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                                                 GlyValValThrValThrGlnAspSerSerLeuGlnAspGlyCysPheIleTyrLysVal 122
                                                                                                                                                                                                                                                                                                 AsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGlyHisAsn 42
LysPheIleGlyValAsnPheProSerAspGlyProValMetGlnLysLysThrMetGly 142
                           GGCGTGGTGACCCAGGACTCCTCCCTGCAGGACGGCACGCTGATCTACAAGGTG
                                                                                             AAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGC
                                                                                                             LysLysLeuSerPheProGluGlyPheLysTrpGluArgValMetAsnPheGluAspGly 102
                                                                                                                                                           CCCCAGTTCCAGTACGGCTCCAAGGCGTACGTGAAGCACCCCGCCGACATCCCCGACTAC
                                                                                                                                                                          ProGlnPheGlnTyrGlySerLysValTyrValLysHisProAlaAspIleProAspTyr 82
                                                                                                                                                                                                                        ACCGCCAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCC
                                                                                                                                                                                                                                           ThrValLysLeuLysValThrLysGlyGlyProLeuProPheAlaTrpAspIleLeuSer 62
                                                                                                                                                                                                                                                                                    AACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCCCTACGAGGGCACCCAG
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1121.00
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Matches:
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APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
TITLE OF INVENTION: FOR MAKING SAME
FILE REFERENCE: UC983.1CP2CP2
CURRENT APPLICATION NUMBER: US/10/209,208
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/121,258
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-05-24
PRIOR PRIOR PRIOR DATE: 2001-05-26
PRIOR FILING DATE: 2001-
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; ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Polunuclec
; OTHER INFORMATION: "mRFP1"
US-10-209-208-9
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US-10-209-208-9
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LENGTH: 678
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Publication No. US20050244921A1
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                                                                                                                        ThrValAsnGlyHisGluPheGluIleGluGlyGluGlyGluGlyArgProTyrGluGly 40
                                                                                                                                                                                                       ATGGCCTCCTCCGAGGACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGC
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                                                                                       TCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCCCTACGAGGGC
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IENGTH: 678

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polunucleoti
OTHER INFORMATION: "mRFFT1"
US-11-218-880-9
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CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION UNMBER: US/10/121,258
PRIOR APPLICATION UNMBER: US/10/121,258
PRIOR APPLICATION UNMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-26
PRIOR APPLICATION UNMBER: 09/866,538
PRIOR APPLICATION UNMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/11218880 Publication No. US20060003420A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC
TITLE OF INVENTION: PROTEIN VARIANTS AND
FILE REFERENCE: UC083.1CP2CP1
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; Publication No. US20050244921A1
; GENERAL INFORMATION OF
APPLICANT: Testen, Roger
; APPLICANT: Geoffrey Baird
TITLE OF INVENTION: FOR MAKING SAME
FILLE REFERENCE: UC083.1CP2CP2
; CURRENT APPLICATION NUMBER: US/10/209,208
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/121,258
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
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